062683 P36568 Q01856 P44499 P22425	64.5 10.9 520 1 LYC_CLOPE P26836 clostridiscope 64.5 10.9 520 1 LYC_CLOPE P26836 clostridiscope 64.5 10.9 659 1 AMIA_STRPN P18791 streptoco 64.0 10.8 359 1 YKA7_CAREL P34258 caenorinal	64 10.8 43.3 1 DHOM_BACSU 64 10.8 803 1 CDAA_BACTU	ALIGNMENTS	SULT 1 OR_HUMAN	1D OTOK HOMAN STANDARD; PKT; 128 AA. AC QSNRC9; AC COMPANDARD; AC	10-UCI-ZUOI (Rel. 40, CIFCATED) 16-UCI-2001 (Rel. 40, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update)	DE OTOTAPLIN PREQUESOR (FIDROCYTE-GETIVEG PROCEIN) (MELANOMA INNIDITORY DE ACTIVITY like protein). GN OTOR OR FDP OR MIAL. OS Homo sapiens (Human).				RA Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.; RT "A novel conserved cochlear gene, OTOR: identification, expression RT analysis, and chromosomal mapping.":		RN 143 RY SEQUENCE FROM N.A. RX MEDLINE-20568254; PubMed=10998416; RA Cohen-Salmon M., Frenz D., Liu W., Verpy E., Voegeling S., Petit C.;				MEDLINE-21100875; Pubmed-11161796; Rendtorff N.D., Frodin M., Attie-Bitach	RI IDENLITICATION and CHARACTERIZATION OF AN INNEL EAR EARLESSED HOMAN RT melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent RT molymorphism that abolishes translation.":	R. Genomics 71:40-52(2001).	RP SEQUENCE FROM N.A. RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,	RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L., RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,	RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., RA Buck D., Burrill W., Butler A.P., Carder C., Carter N.P.,	RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,	RA Coulson A., Coville G.J., Deadman R., Dhami P., Dunn M.,	RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,	RA Hammond S., Harley J.L., Hearn P.D., HO S., Holden J.L., Howden P.J., , RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,	RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S., RA Lehvaslaiho M.H., Leversha M., Lloyd C., Lloyd D.M., Lovell J.D.,	
GenCore v	Om protein - protein search, using sw mode. Run on: September 23, 2002, 09:37:55; Search time 11.82 Seconds (without alignments) 360.334 Million cell updates/sec	Title: US-10-019-455A-24 Perfect score: 590 Sequence: HGIFMDRLASKRLCADDECVRVYQEATKEVPTTDIDFFCE 110	Scoring table: BLOSUM62 Gapext 0.5	seds,	cal number of hits satisfying chosen parameters: 105224	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : SwissProt_40:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES	Result Ouery Ouery Date In Description	SCOTE MACCII LENGULI DE 10	390 100.0 128 1 OTOR_MOUSE Q91ie3 mus m 477.5 80.9 132 1 OTOR_CHICK Q91ie3 mus m 390 66.1 133 1 OTOR_RANCA Q91i8p5 rana	43.0 131 1 MIA_HUMAN 42.8 130 1 MIA_BOVIN 42.5 130 1 MIA_RAT	235.51 39.9 130 1 MIA MOUSE Q61865 88.5 15.0 847 1 VAV3_MOUSE Q9r0c8 m	86.5 14.7 845 1 VAV_HUMAN P15498 h • 86.5 14.7 847 1 VAV3_HUMAN Q9ukw4 h	85.5 14.5 843 1 VAV_RAT P54100 r	22.5 14.0 666 1 81.5 13.8 878 1 78.5 13.3 1589 1	72 12.2 520 1 TEN_HUMAN 015811 h 71.5 12.1 541 1 ASNH METJA 058516 m	70.5 11.9 905 1 203_MOUSE 099xy1 69 11.7 392 1 RURE ACICA P42454	69 11.7 444 1 PURZ_METJA 058347 69 11.7 670 1 XBXZ SCHPO 010199	68.5 11.6 505 1 SRK1_SPOLA P42686 5 68.5 11.6 506 1 SRK4_SPOLA P42690 s	68 11.5 162 1 BAR2_CHIPA P08725 (68 11.5 534 1 VL2_HPV37 Q80905 h	67 11.4 509 1 SYE/VIBCH 031153 V	67 11.4 524 1 VL2_HPV17	66 11.2 326 1 BAR1_CHIPA P08724 C 66 11.2 518 1 VL2_HPV36 P50827 h	

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NCBI_TaxID=9031;
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Q918P6;
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                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                  Milne S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H., Rice C.M., Ross M.T., Soder C.E., Sehra H.K., Shownkeen R., Sims S., Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E., Swann M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Whitchead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A., Rogers J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                               sequence and comparative analysis of human chromosome 20.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A., Milne S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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01-MAR-2002 (Rel. 41, Last annotation update)
Otoraplin precursor (Melanoma inhibitory activity-like protein).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GEFWAGSVYGDGQDEMGVVGYFPRNLVKEQRVYQEATKEVPTTDIDFFCE 110
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                                                                                                                                                                                                                                                               Nature 414:865-871(2001).

-: SUBCELLULAR LOCATION: Secreted (Potential).

-: TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COCHLEA.

-: SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.

-: SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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SIMILARITY.
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EMBL, A7243505; AAG42356.1; --
EMBL, A7245522, CAC27443.1; --
EMBL, A7252324; CAC28085.1; --
EMBL, A7252325; CAC28085.1; --
EMBL, A7252325; CAC28085.1; JOINED.
EMBL, A7252327; CAC28085.1; JOINED.
EMBL, A7352327; CAC28085.1; JOINED.
EMBL, A7343438; CAC16848.1; --
MIN; 606067; --
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SMART; SM00326; SH3; 1.
PROSITE; PS50002; SH3; FALSE_NEG.
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39
32
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128 AA;
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es 110; Conser
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SIGNAL
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Q9JIE3;
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-20334619; PubMed-10873378; Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S., Denis C.S., Bell A.M., Hudspelh A.J., Morton C.C.; "A novel conserved cochlear gene, OTOR: identification, expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 128;
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3DD47D4C77C4A7FD CRC64;
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Pred. No. 2.3e-50;
7; Mismatches 4;
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16-0CT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
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                                                                                  analysis, and chromosomal mapping."; Genomics 66:242-248(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY
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Best Local Similarity 90.0%;
Matches 99; Conservative 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELICETPRO: IPRO01452; SH3.
SMART; SM00326; SH3; 1.
PROSITE; PS50002; SH3; 1.
Signal; SH3 domain.
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128
110
37
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Strausberg R.
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Q16674;
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                                                                                                                                                                                                                                   Query Match
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Matches 6
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                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 GIFMDKLASKKLCADDDCVYTISLVRAEEDYNAPDCRFINIKKGQLIYVYSKLVKEKESG 82
SEQUENCE FROM N.A.
MEDLINE=2034619; PubMed=10873778;
Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S., Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.;
"A novel conserved cochlear gene, OTOR: identification, expression analysis, and circosomal mapping.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
Ranidae; Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                ij
                                                                                                                                                                                                                                                                                                                                                                                                     80.9%; Score 477.5; DB 1; Length 132; 80.0%; Pred. No. 4.3e-43; ive 9; Mismatches 12; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 EFWAGSVYGDG-QDEMGVVGYFPRNLVKEQRVYQEATKEVPTTDIDFFCE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY.
SIMILARITY.
9DICB07FD353CE1C CRC64;
                                                           analysis, and chromosomal mapping.";
Genomics [66.242-248(2000).
--- SUBCELLULIAR LOCATION: Secreted (Potential).
--- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COCHLEA.
--- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
--- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rana satesbeiana (Bull frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTOR FAMILY.
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16-CCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
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OTORAPLIN.
SH3.
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                                                                                                                                                                                                                                                                                                                                                      131
                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Otoraplin precursor.
                                                                                                                                                                                                                                                                                             Signal; SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                   132 AA;
                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
es 88; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-8400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTOR_RANCA
Q918P5;
                                                                                                                                                                                                                                                                                                                                           DISULFID
DISULFID
SEQUENCE
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Matches
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKEN-G 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95007612; PubMed=7923218;
Blesch A., Bosserhoff A.-K., Apfel R., Behl C., Hessdoerfer B.,
Schmitt A., Jachimczak P., Lottspeich F., Buettner R., Bogdahn U.;
"Cloning of a novel malignant melanoma-derived growth-regulatory
protein, MIA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Placenta;
MEDINE-96132947; PubMed-8550608;
MEDINE-96132947; PubMed-8550608;
Bosserhoff A.-K., Hein R., Bogdahn U., Buettner R.;
"Structure and prompter analysis of the gene encoding the human melanoma-inhibiting protein MIA.";
J. Biol. Chem. 271:490-495(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (1.39 ANGSTROMS) OF 25-131.
MEDLINE-21244635; PubMed=11331761;
Lougheed J.C., Holton J.M., Alber T., Bazan J.F., Handel T.M.;
"Structure of melanoma inhibitory activity protein, a member of recently identified family of secreted proteins.";
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NNY-2002 (Rel. 41, Last annotation update)
Melanoma derived growth regulatory protein precursor (Melanoma inhibitory activity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 AGEFWAGSVYGDG-QDEMGVVGYFPRNLVKEQRVYQEATKEVPTTDIDFFCE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.1%; Score 390; DB 1; Length 133; 58.9%; Pred. No. 6e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                               // SIMILARITY.
// SIMILARITY.
25440C1A3CF911AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                          OTORAPLIN.
                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                 EMBL; AF233519; AAF82728.1; -.
InterPro; IPRO01452; SH3.
SMART; SM00326; SH3; 1.
PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                          23 PO
133 OT
115 SH
40 BY
132 BY
15243 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein, MIA.";
Cancer Res. 54:5695-5701(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens (Human)
                                                                                                                                                                                                                                                                                                                                       24 1
48 1
35
58 1
133 AA;
                                                                                                                                                                                                                                                                                   Signal; SH3 domain. SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dietz U.H., Sandell L.J.; "Cloning of a retinoic acid-sensitive mRNA expressed in cartilage and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 MDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGE-F 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-Mara-2002 (Rel. 41, Last annotation update)
Melanoma derived growth regulatory protein precursor (Melanoma inhibitory activity) (Cartilage-derived retinolc acid-sensitive protein) (CD-RAP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Gene expression changes associated with chemically-induced rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
MELANOMA DERIVED GROWTH REGULATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 WAGSV----YGDGQDEMGVVGYFPRNLVKEQRVYQEATKEVPTTDIDFFCE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: MAY FUNCTION DURING CARTILAGE DEVELOPMENT AND
                    MAINTENANCE.

- SUBCELLULAR LOCATION: Secreted.

- TISSUE SPECIFICITY: CARTILAGE PRIMORDIA AND CARTILAGE.

- INDUCTION: REPRESSED BY RETINOIC ACID.

- PTM: MAY POSSESS TWO INTRAMOLECULAR DISULFIDE BONDS.

- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.

- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
BY SIMILARITY.
95D153161C78E02A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.8%; Score 252.5; DB 1;
45.0%; Pred. No. 1.4e-19;
tive 22; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-Mammary gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                              domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Cartilage;
MEDLINE-96216414; Pubmed-8621736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14353 MW;
                                                                                                                                                                                                                                                                                                                                           EMBL; U51437; AAC48523.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 34-124 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001452; SH3.
Pfam; PF00018; SH3; 1.
SMART; SM00326; SH3; 1.
PROSITE: PS50002; SH3; 1.
Growth factor; Signal; SH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112
40
129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42
35
58
130 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 50; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIA_RAT
Q62946; P97591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIA OR CDRAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
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Dietz U.H., Sandell L.J.;
"Cloning of a retinocacid-sensitive mRNA expressed in cartilage and
during chondrosenesis.";
                -1- FUNCTION: ELICITS GROWTH INHIBITION ON MELANOMA CELLS IN VITRO
AS WELL AS SOME OTHER NEUROBETOBERMAL TUMORS, INCLUDING GLIOMAS.
-1- SUBCELLULAR LOCATION: Secreted.
-1- TISSUE SPECIFICITY: ALL MALIGNANT MELANOMA CELL LINES TESTED AND INFREQUENTLY IN GLIOMA CELL LINES.
-1- PTM: MAY POSSESS TWO INTRAMOLECULAR DISULFIDE BONDS.
-1- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
-1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NAR-2002 (Rel. 41, Last annotation update)
Melanoma derived growth regulatory protein precursor (Melanoma inhibitory activity) (Cartilage-derived retinoic acid-sensitive protein) (CD-RAP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MELANOMA DERIVED GROWTH REGULATORY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 WAGSVYGDGQDEMGV-VGYFPRNLVKEQRVYQEATKEVPTTDIDFFCE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 253.5; DB 1;
Pred. No. 1.1e-19;
Sci. U.S.A. 98:5515-5520(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            domain; 3D-structure.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21; Mismatches
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SH3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    during chondrogenesis.";
J. Biol. Chem. 271:3311-3316(1996).
                                                                                                                                                                                                                                                                                                                                                         EMBL; X84707; CAA53195.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43.0%;
ilarity 45.4%;
Conservative 25
                                                                                                                                                                                                                                                                                                                                                                                        EMBL, BC005910; AAH05910.1; PDB, 111J; 16-MAY-01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00326; SH3; 1.
PROSITE; PS50002; SH3; 1.
Growth factor; Signal; SH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001452; SH3.
Pfam; PF00018; SH3; 1.
SMART; SM00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43
36
59
131 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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Q28038;
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SEQUENCE
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MIA_BOVIN

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Gaps

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Indels

Length 130;

DB 1;

82

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130 AA;
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[1]
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35
58
112
                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VAV-3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VAV3_MOUSE
Q9R0C8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                           Growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
VAV3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VAV3
     ID DT DT DT DT OC OC OC OC OX
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                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 MDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGE-F 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blesch A., Bosserhoff A.-K., Apfel R., Behl C., Hessdoerfer B., Schmitt A., Jachimczak P., Lottspelch F., Buettner R., Bogdahn U., Cloning of a novel malignant melanoma-derived growth-regulatory protein, MIA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 MPKLADRKLCADEECSHPISMAVALQDYVAPDCRFLTIYRGQVVYVFSKL--KGRGRLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBL_FaxIp=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIA_MOUSE STANDARD, PRT; 130 AA.
061865; P97495; 009086;
01.NOV-1997 (Rel. 35, Created)
16.OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Melanoma derived growth regulatory protein precursor (Melanoma inhibitory activity) (Cartilage-derived retinoic acid-sensitive
                                                                                                                                                                                                                                                                                                                             POTENTIAL.
MELANOMA DERIVED GROWTH REGULATORY PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 130;
               J. Biol. Chem. 271:3311-3316(1996).
-!- FUNCTION: MAY FUNCTION DURING CARTILAGE DEVELOPMENT AND
                                                -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: CARTILAGE PRIMORDIA AND CARTILAGE.
-!- INDUCTION: REPRESSED BY RETINOIC ACID.
-!- PTM: MAY POSSESS TWO INTRAMOLECULAR DISULFIDE BONDS.
-!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 WAGSVYGDGQDEMGV-VGYFPRNLVKEQRVYQEATKEVPTTDIDFFCE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 WGGSVQGDYYGDLAAHLGYFPSSIVREDLILKPGKVDMKTDEWDFYCQ 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                     1 -> VT (IN REF. 2).
5F99149AECF74501 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.5%; Score 250.5; DB 1;
Ilarity 44.4%; Pred. No. 2.2e-19;
Conservative 23; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
chondrogenesis.";
1. Chem. 271:3311-3316(1996).
                                                                                                                                                                                                                                                  EMBL; U67884; AB40659.1; -...
InterPro | IPR001452; SH3.
Pfam; PF00018; SH3; 1.
SMARTE; SM00326; SH3; 1.
PROSTIE; PS50002; SH3; FALSE_NEG.
Growth factor; Signal; SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BALB/C;
MEDLINE-95007612; Pubmed-7923218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cancer Res. 54:5695-5701(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                  14536 MW;
                                                                                                                                                                                                                                         EMBL; U51438; AAC52481.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                 130 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 48 Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein) (CD-RAP).
MIA OR CDRAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                  42
35
58
46
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DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                          CHAIN
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                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: ALL MALIGNANT MELANOMA CELL LINES TESTED AND INFREQUENTLY IN GLIOMA CELL LINES.
-!- PTM: MAY POSSESS TWO INTEMOLECULAR DISULFIDE BONDS.
-!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
STRAIN=129/SV;
MEDLINE=97521341; PubMed=9097023;
MEDLINE=97521341; PubMed=9097023;
MEDSEAFURE=975251341; PubMed=9097023;
Gilbert D.J., Jenkins N.A., Buettner R., Sandell L.J.;
"Mouse CD-RAP/MIA gene: structure, chromosomal localization, and expression in cartilage and chondrosarcoma.";
Dev. Dyn. 208:516-525(1997).
-!- FUNCTION: ELICITS GROWTH INHIBITION ON MELANOMA CELLS IN VITRO AK SIMELAS SOME OTHER NEUROECTODERMAL TUMORS, INCLUDING GLIOMAS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 MDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGE-F 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MELANOMA DERIVED GROWTH REGULATORY PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39.9%; Score 235.5; DB 1; Length 130; 43.5%; Pred. No. 8.1e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 WAGSVYGDGQDEMGV-VGYFPRNLVKEQRVYQEATKEVPTTDIDFFCE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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16C957459C5BB5F9 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.5%; Pred. ....
tive 21; Mismatches
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BY SIMILAPITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E; PS50002; SH3; FALSE_NEG.
factor; Signal; SH3 domain.
1 22 POTEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14593 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X94322; CAA63983.1; -. EMBL; U8512; AAB42082.1; -. EMBL; X97965; CAA6608.1; -. MGD; MGI.109615; Cdrap. InterPro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00018; SH3; 1.
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3;

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31.3%; Pred. No. 0.14;

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Best Local Similarity
                                 Matches
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                    Trenkle T., McCleiland M., Welsh J.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: EXCHANGE FACTOR FOR GTP-BINDING PROTEINS RHOA, RHOG AND,
TO A LESSER EXTENT, RAC-1. BINDS PHYSICALLY TO THE NUCLEOTIDE-FREE
STATES OF THOSE OFTPASES (BY SIMILARITY).
-!- ALTERNATIVE PRODUCTS: 2 ISOPORMS; ALPHA (SHOWN HERE) AND BETA;
ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                               SIMILARITY: CONTAINS 1 CALPONIN-HOMOLOGY (CH) DOMAIN.
SIMILARITY: CONTAINS 1 DBL-HOMOLOGY DOMAIN (DH).
SIMILARITY: CONTAINS 1 PH DOMAIN.
SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG BINDING DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SH2 domain; SH3 domain; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHORBOL-ESTER AND DAG BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9A6B63F0D9E60F8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00233; PH; 1.
SMART; SM00225; RhoGEF; 1.
SMART; SM00252; SH2; 1.
SMART; SM00256; SH3; 2.
PROSITE; PS50021; CH; 1.
PROSITE; PS50021; CH; 1.
PROSITE; PS50081; DAG_PE_BIND_DOM_1; 1.
PROSITE; PS50010; DH_2; 1.
PROSITE; PS50010; DH_2; 1.
                                                                                                                                                                                                                                                                                                                        SIMILARITY: CONTAINS 1 SH2 DOMAIN. SIMILARITY: CONTAINS 2 SH3 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:1888518; Vav3.
InterPro; IPR003247; CH_type.
InterPro; IPR001715; Calponin_hom.
InterPro; IPR001315; Calponin_hom.
InterPro; IPR001331; GDS_CDC24.
InterPro; IPR001849; PH.
InterPro; IPR001849; PH.
InterPro; IPR001895; SH3.
InterPro; IPR001865; SH3.
InterPro; IPR001852; SH3.
InterPro; IPR001852; SH3.
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PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF067816; AAF09171.1; -. HSSP; P12931; 1A1E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00307; CH; 1.
Pfam; PF00130; DAG_PE-bind; 1.
Pfam; PF00169; PH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR00888; SM22CALPONIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97946 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00621; RhoGEF; 1.
Pfam; PF00017; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom; PD001527; CH_t
SMART; SM00109; Cl; I.
SMART; SM00033; CH; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 788
847 AA;
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SEQUENCE
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DOMAIN
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Length 847;

DB 1;

Score 88.5;

15.0%;

Query Match

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Ramos-Morales F., Romero F., Schweighoffer F., Bismuth G., Camonis J., Tortolero M., Fischer S., "The proline-rich region of Vav binds to Grb2 and Grb3-3."; Oncogene 11:1665-1669(1995).
                                                                                                          TRUNCATION OF THE N-TERMINUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Katzav S., Cleveland J.L., Heslop H.E., Pulido D.;
"Loss of the anino-terminal helix-loop-helix domain of the vav proto-
oncogene activates its transforming potential.";
Mol. Cell. Biol. 11:1912-1920(1991).
       11; Gaps
                                                                23 ISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYF 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

Denkinger D.J., Borges C.R., Shaw C.L., Cushman A.M., Kawahara R.S.;
"Transcriptional regulation of the vav proto-oncogene.";
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-92228488; PubMed-1565462; Adams J.M., Houston H., Allen J., Lints T., Harvey R.; Adams J.M., Houston H., Allen J., Lints T., Harvey R.; "The hematopoietically expressed vav proto-oncogene shares homology with the dbl GDP-GTP exchange factor, the bor gene and a yeast gene (CDC24) involved in cytoskeletal organization."; Oncogene 7:618(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BINDING PROTEIN. CAN BE ACTIVATED BY TRUNCATION OF THE N-TERMIN -!- TISSUE SPECIFICITY: WIDELY EXPRESSED IN HEMATOPOIETIC CELLS BUT NOT IN OTHER CELL TYPES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- FUNCTION: PROBABLE EXCHANGE FACTOR FOR A SMALL RAS-LIKE GTP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -:- SIMILARITY: CONTAINS 1 CALPONIN-HOMOLOGY (CH) DOMAIN.
-:- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY DOMAIN (DH).
-:- SIMILARITY: CONTAINS 1 PH DOMAIN.
-:- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 62-845 FROM N.A.
MEDLINE=90005432; PubMed=2477241;
Katzav S., Martin-Zanca D., Barbacid M.;
'vav, a novel human oncogene derived from a locus ubiquitously expressed in hematopoletic cells.";
EMBO J. 8:2283-2290(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
21; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 1 SH2 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-61 FROM N.A. MEDLINE=91172176; PubMed=2005887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 299-334 FROM N.A. MEDLINE=96038895; PubMed=7478592;
                                                                                                                                                                                                                                                                                                                                                                                                                                        VAV_HUMAN STANDARD; PRIP15498; 015860; 14. Created) 16-OCT-2001 (Rel. 40, Last sequent) 1-MAR-2002 (Rel. 41, Last annots VAV proto-oncogene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 299-837 FROM N.A.
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                                                                                                                                                                                                                                                                           839 PSTYVEE 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                    83 PRNLVKE 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Romero F.
                                                                                                                                                                                                                                                                                                                                                                                                               VAV_HUMAN
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TISSUE SECURITE FROM N.A.

TISSUE-Breast, and Colon carcinoma;

MEDLINE-98371222; bubMed=9705494;

MEDLINE-98371222; bubMed=9705494;

AT Trenkle T., Welsh J., Jung B., Mathieu-Daude F., McClelland M.;

TO A LESS TO TRANCE FACTOR FOR GTP-BINDING PROTEINS RHOA, RHOG AND,

TO A LESSER EXTENT, RAC-1. BINDS PHYSICALLY TO THE NUCLEOTIDE-FREE
STRATES OF THOSE GTPASES.

TO A LESSER EXTENT, RAC-1. BINDS PHYSICALLY TO THE NUCLEOTIDE-FREE
STRATES OF THOSE GTPASES.

ARE PRODUCED BY ALTERNATIVE SPLICING.

-1- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY DOMAIN (DH).

-1- SIMILARITY: CONTAINS 1 PLOWALIN.

-1- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG

-1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.

-1- SIMILARITY: CONTAINS 2 SH3 DOMAIN.

-1- SIMILARITY: CONTAINS 2 SH3 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
PROSITE; PS50100; DHL2; 1.
PROSITE; PS50003; PH_2; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 2.
PROFICE; PS50002; SH3; 2.
PROFICE; PSF0002; SH3; 2.
PROFICE; PSF00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21; Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 ASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYFPRN 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DECURING FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE-99455043; PubMed=10523675;
Movilla N., Bustelo X.R.;
"Biological and regulatory properties of Vav-3, a new member of the Vav family of oncoproteins.";
Mol. Cell. Biol. 19:7870-7885(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Wasaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 14.7%; Score 86.5; DB 1; Length 845; Best Local Similarity 32.9%; Pred. No. 0.23;
                                                                                                                                                                                                                                                                                                                                                          PHORBOL-ESTER AND DAG BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A -> P (IN REF. 2).
I -> TV (IN REF. 2).
AC3BC9736FD2F138 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OVAV3_HUMAN STANDARD; PRT; 847 AA. 0910KM4; 095230; 09Y5X8; 16-CT-2001 (Rel. 40, Created) 16-CT-2001 (Rel. 40, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     SH3 1.
                                                                                                                                                                                                                                                                                                                                                                                                                    SH2.
SH3 2.
                                                                                                                                                                                                                                                                                                   DH.
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3373
504
564
660
765
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402
516
617
671
782
264
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836 YVEED--YSE 843
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CONFLICT
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DOMAIN
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                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
   !- SIMILARITY: CONTAINS 2 SH3 DOMAINS.
!- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN IN POSITIONS 322
                                                                                                                                                                                                                                                                                                                                                                               1), JOINED.
1), JO
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1; JOINED.
1; JOINED.
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EMBL; M59834; AAA63267.1; -.
EMBL; X83931; CAA58783.1; -.
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IPR003096; SM22_calponin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AF030223, AAC25011.1; JOINED
EMBL, AF030224, AAC25011.1; JOINED.
EMBL, AF030225, AAC25011.1; JOINED.
EMBL, AF030226, AAC25011.1; JOINED.
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Calponin_hom..
DAG_PE-bind.
                                                                  TO 355 DUE TO A FRAMESHIFT.
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Pfam; PF00130; DAG_PE-bind; 1.
Pfam; PF00169; PH; 1.
Pfam; PF00621; RhoGEF; 1.
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PD001527; CH_type; 1.
                                                                                                                                                                                                                                                                                                                                                       EMBL; AF03027; AAC25011.1; -.
EMBL; AF030201; AAC25011.1; JC
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SWART; SW00109; Cl; I.
SWART; SW00033; CH; I.
SWART; SW00233; PH; I.
SWART; SW00325; RhoGEF; I.
SWART; SW00325; RH2; I.
SWART; SW00326; SH3; I.
SWART; SW00326; SH3; I.
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PRINTS; PR00452; SH3DOMAIN.
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AAC25011.1
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Pfam; PF00018; SH3; 2.
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InterPro; IPR001715;
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PIR; B39576; B39576.
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TRANSFAC; T00880; -.
MIM; 164875; -.
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InterPro;
InterPro;
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InterPro;
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790 LGIAIARYDFCARDMRELSLLKGDVVKIYTKM----SANGWWRGEVNGR-----VGWF 838

83 PRNLVKE 89

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LLCQLLNNLRAHSINLKEINLRPQMSQFLCLKNIRTFLTAC
CETFGMRKSELFEAPDLFDVRDFGK -> MQLPDCPCRAHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phorbol-ester binding; Zinc; SH2 domain; SH3 domain; Repeat;
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K -> E (IN REF. 2).

Y -> H (IN REF. 1; AAD20348).

T -> S (IN REF. 2).

V -> A (IN REF. 1; AAD20348).

W; ClE29F0B094CB721 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               factor; Alternative splicing
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PROSITE; PSS00479; DAG_PE_BIND_DOM_1; 1.
PROSITE; PSS0041; DAG_PE_BIND_DOM_2; 1.
PROSITE; PSS0010; DH_2; 1.
PROSITE; PSS00741; DH_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001849; PH.
InterPro; IPR000119; RhGEF.
InterPro; IPR000980; SH2.
InterPro; IPR001452; SH3.
InterPro; IPR003996; SM22_calponin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SH2.
SH3 2.
                                                                                                                                                                                                                                                                                                                                                                      MIM; 605541; -
Interpro; IPR003247; CH_type.
Interpro; IPR001715; Calponin_hom
Interpro; IPR002219; DAG_PE-bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50003; PH_DOMAIN; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 2.
                                                                                                                                                                                                                                                     EMBL; AF118887; AAD20349.1; -.
EMBL; AF118886; AAD20348.1; -.
EMBL; AF067817; AAC79695.1; -.
HSSP; P12931; IALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001331; GDS_CDC24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00307; CH; 1.
Pfam; PF00130; DAG_PE-bind; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CH_type; 1.
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PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR00888; SM22CALPON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00233; PH; 1.
SMART; SM00325; RhoGEF; 1.
SMART; SM00252; SH2; 1.
SMART; SM00326; SH3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00169; PH; 1.
Pfam; PF00621; RhoGEF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00109; C1; 1
SMART; SM00109; C1; 1
SMART; SM00033; CH; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00017; SH2; 1
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217
298
429
847 AA;
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Pfam; PF00169;
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CONFLICT
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                          01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
VAVI OR VAV.
                                                                                                                                                                                                   843 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BINDING DOMAIN.
-!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-!- SIMILARITY: CONTAINS 2 SH3 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##SSP, P29354, i.GRI.
##SSP, P29354, i.GRI.
InterPro; IPR003247; CH_type.
##InterPro; IPR001715; Calponin_hom.
### InterPro; IPR001715; DAG_PE-bind.
### InterPro; IPR001849; PM.
### InterPro; IPR00180; SH2.
### InterPro; IPR00180; SH3.
#### InterPro; IPR00180; SH3.
### InterPro; IPR00180; SH3.
### InterPro; IPR00180; SH3.
### InterPro; IPR00180; SH3.
#### InterPro; IPR00180; SH3.
##### InterPro; IPR00180; SH3.
#### InterPro; IPR00180; SH3.
##### InterPro; IPR00180; SH3.
##### InterPro; IPR00180; IPR00180; IPR00180; IPR00180; IPR00
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PROSITE; PS00479; DAG_PE_BIND_DOM_1;
PROSITE; PS50081; DAG_PE_BIND_DOM_2;
PROSITE; PS50010; DH_2; 1.
                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS00741; DH_1; 1.
PS50003; PH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS,
PRO0452; SHICKLEY
PRODOM; PD001527; CH_type; 1.
SMART; SM00109; C1; 1.
SMART; SM0033; CH; 1.
SMART; SM0023; PH; 1.
R SMART; SM0025; RhGGE; 1.
R SMART; SM0025; RhGGE; 1.
R SMART; SM00325; RhGGE; 1.
                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
839 PSTYVEE 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
PROSITE;
PROSITE;
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5

11; Gaps

21; Indels

23 ISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYF 82

:: :: ::

21; Conservative

Matches •

δ

Local Similarity

Query Match

14.7%; Score 86.5; DB 1; Length 847; 31.3%; Pred. No. 0.23; Live 14; Mismatches 21; Indels 1

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or send an email to license@isb-sib.ch).
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845 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 LVKEQRVYQE 95
                                                                                                                                                                                                                                                                                                                                                                                                    PS50001;
PS50002;
                                                                                                                                                                                                                                                                                                                                                                                          PS50003;
                                                                                                                                                                                                                                                                                                                                                                               PS00741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997
01-NOV-1997
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VAV2_MOUSE
Q60992;
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PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
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                                                                                                                                                                                                                                                                                 SMART;
SMART;
SMART;
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VAV2_MOUSE
                                                                                                                                                                                       Pfam;
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                                                                                                                                                                   3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                     26 ASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYFPRN 85
PROSITE; PS50001; SH2; 1.
PROSITE; PS5002; SH3; 2.
Proto-oncogene; Phorbbol-ester binding; Zinc; SH2 domain; SH3 domain; Guanine-nycleotide releasing factor; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adams J.A, Houston H., Allen J., Lints T., Harvey R.; "The hematopoietically expressed vav proto-oncogene shares homology with the dbl GDP-GTP exchange factor, the bcr gene and a yeast gene (CDC24) involved in cytoskeletal organization.";
                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -:- SIMILARITY: CONTAINS 1 CALPONIN-HOMOLOGY (CH) DOMAIN.
-:- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY DOMAIN (DH).
-:- SIMILARITY: CONTAINS 1 PH DOMAIN.
-:- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
                                                                                                                                                                   13,
                                                                                                                                             14.5%; Score 85.5; DB 1; Length 843; 31.4%; Pred. No. 0.29; ive 14; Mismatches 21; Indels 1
                                                                      PHORBOL-ESTER AND DAG BINDING SH3 1. SH2.
                                                                                                                C4A5CACD45FCB80E CRC64;
                                                                                                                                                                                                                                                                                                                       01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                       845 AA
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-!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-!- SIMILARITY: CONTAINS 2 SH3 DOMAINS.
                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE-92228488; PubMed-1565462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91172176; PubMed=2005887;
                                                                                                                97953 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [2] |
SEQUENCE OF 1-93 FROM N.A.
                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                             Query Match |
Best Local Similarity
Matches 22; Conserva
                                                                                                                                                                                                                                                                                                                                                       VAV proto oncogene.
                                                                                                                                                                                                                                                  --YSE 841
                                                                                                              843 AA;
                                                                                                                                                                                                                             86 LVKEQRVYQE 95
                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                     VAV_MOUSE
P27870;
                                                                                                                                                                                                                                                  834 YVEED
                                                                                                                SEQUENCE
                                                                                            DOMAIN
                                          DOMAIN
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proto-oncogene; Phorbol-ester binding; Zinc; SH2 domain; SH3 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHORBOL-ESTER AND DAG BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q -> E (IN REF. 2).
366DCCD1C5229DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.5%; Score 85.5; DB 1;
31.4%; Pred. No. 0.29;
tive 14; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guanine-nucleotide releasing factor; Repeat DOMAIN 1 119 CH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS5001; CH; 1.
PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
PROSITE; PS50010; DH_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SH3 1.
SH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SH3 2.
                                                                                                                                                                 Calponin_hom.
DAG_PE-bind.
GDS_CDC24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DH_1; 1.
PH_DOMAIN; 1.
SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 35, Created)
(Rel. 35, Last sequ
(Rel. 41, Last anno
                                                                                                                                                                                                     Interpro; IPR001331; GDS_CDC24
Interpro; IPR001849; PH.
Interpro; IPR000219; RhoGEF.
Interpro; IPR000980; SH2.
Interpro; IPR001452; SH3.
Pfam; PF00307; CH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 Q
98136 MW;
                                                                                                                                                                                                                                                                                                      PF00307; CH; 1.
PF00130; DAG_PE-bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0008; DAGPEDOMAIN.
PRINTS; PRO0452; SH3DOMAIN.
ProDom; PD001527; CH_type; 1.
                                                                                                                                                   CH_type.
EMBL; X64361; CAA45713.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00233; PH; 1.
SMART; SM00325; RhoGEF; 1.
SMART; SM00252; SH2; 1.
SMART; SM00326; SH3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22; Conservative
                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00621; RhoGEF; 1. Pfam; PF00017; SH2; 1. Pfam; PF00018; SH3; 2.
                                  AAA63402.1;
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                                              PIR; A39576, A39576.
PIR; S36941, S36941.
HSSP; P29554, IGRI.
TRANSFAC; T01230; --
MGD; MGI:98923; Vav.
InterPro; IPR003247; CI
InterPro; IPR001715; CZ
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DOMAIN
            DOMAIN
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                                                                                                          STRAIN-C57BL/6;
MEDLINE-96313271; PubMed-8710375;
Schuebel K.E., Bustelo X.R., Nielsen D.A., Song B.J., Barbacid M.,
                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                   -: SIMILARITY: CONTAINS 1 CALPONIN-HOMOLOGY (CH) DOMAIN.
-: SIMILARITY: CONTAINS 1 DBL-HOMOLOGY DOMAIN (DH).
-: SIMILARITY: CONTAINS 1 PH DOMAIN.
-: SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG BINDING DOMAIN.
-: SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-: SIMILARITY: CONTAINS 2 SH3 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DH.
PH.
PH.
SH3 1.
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Phorbol-ester binding; Zinc; SH2 domain; SH3 domain;
Guanine-nucleotide releasing factor; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00326; SMC, 1.

PROSITE; PS50021; CH; 1.

PROSITE; PS500479; DAG_PE_BIND_DOM_1; 1.

PROSITE; PS50010; DH 2; 1.

PROSITE; PS50010; DH 2; 1.
                                                                                                                                                                                                                                                                                                                                             MGD; MGI:102718; Vav2.
InterPro; IPR001247; CH_type.
InterPro; IPR001715; Calpoini_hom.
InterPro; IPR001319; DAG_PE-bind.
InterPro; IPR001331; GDS_CDC24.
InterPro; IPR001849; PH.
InterPro; IPR000819; RhoGEF.
InterPro; IPR00080980; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS50003; PH_DOMAIN; 1. PS50001; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00307; CH; 1.
Pfam; PF00130; DAG_PE-bind; 1.
Pfam; PF00169; PH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00017; SH2; 1.
Pfam; PF00018; SH3; 2.
PRINTS; PR00452; SH3DOMAIN.
ProDom; PD001527; CH_type; 1.
SMART; SM00109; C1; 1.
                                                                                                                                                                                                                                                                                                                           EMBL; U37017; AAC52761.1; -.
HSSP; Q60631; 1GBQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00325; RhoGEF; 1.
SMART; SM00252; SH2; 1.
SMART; SM00326; SH3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00621; RhoGEF; 1.
                                                                                                                                                           BINDING PROTEIN
                                                                    SEQUENCE FROM N.A.
                                                NCBI_TaxID-10090;
VAV-2 protein.
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PROSITE;
PROSITE;
PROSITE;
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DOMAIN
DOMAIN
DOMAIN
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SMART;
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                                                                                                                                                                                                                                                                                           13; Gaps
                                                                                                                                                                                                                                                        20 VYT---ISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEM 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-95283235; PubMed-7762982; Henske E.P., Short M.P., Jozwiak S., Bovey C.M., Ramlakhan S., Haines J.L., Kwiatkovski D.J.; Haines J.L., Kwiatkovski D.J.; "Identification of VAV2 on 9q34 and its exclusion as the tuberous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sclerosis gene TSC1.";
Ann. Hum. Genet. 59:25-37(1995).
-!- FUNCTION: PROBABLE EXCHANGE FACTOR FOR A SMALL RAS-LIKE GTP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BINDING PROTEIN.

-! SIMILARITY: CONTAINS 1 CALPONIN-HOMOLOGY (CH) DOMAIN.
-! SIMILARITY: CONTAINS 1 DBL-HOMOLOGY DOMAIN (DH).
-! SIMILARITY: CONTAINS 1 PH DOMAIN.
-! SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG BINDING DOMAIN.
-! SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-! SIMILARITY: CONTAINS 2 SH3 DOMAINS.
                                                                                                                                       Query Match 14.0%; Score 82.5; DB 1; Length 868; Best Local Similarity 27.6%; Pred. No. 0.61; Matches 21; Conservative 20; Mismatches 22; Indels 1.
                                                        99915 MW; D18581E7EEB2DBC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
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Calponin_hom.
DAG_PE-bind.
GDS_CDC24.
                                SH3
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PF00130; DAG_PE-bind; 1.
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InterPro; IPR001331; GDS_CC
InterPro; IPR001849; PH.
InterPro; IPR000218; RhoGEE
InterPro; IPR000980; SH2.
InterPro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                        | :|:|| |:|: |
852 GRIGWEPSTYVEEEGV 867
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                                                                                                                                                                                                                                                                                                                                                                     77 GVVGYFPRNLVKEQRV 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003247;
InterPro; IPR001715;
663
806
868 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00169;
PF00621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VAV-2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VAV2_HUMAN
P52735;
                                                        SEQUENCE
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Query Match 13.8%; Score 81.5; DB 1; Length 878; Best Local Similarity 26.3%; Pred. No. 0.78; Matches 20; Conservative 21; Mismatches 22; Indels 13; Gaps
Pfam; PF00017; SH2; 1.

Pfam; PF00018; SH3; 2.

Price Pfam; PF00018; SH3; 2.

Proban; PR001527; CH_type; 1.

SMART; SM0019; C1; 1.

SMART; SM0033; CH; 1.

SMART; SM0033; CH; 1.

SMART; SM00325; RhoGEF; 1.

SMART; SM00325; RhoGEF; 1.

SMART; SM00325; SH2; 1.

PROSITE; PS0001; CH; 1.

PROSITE; PS0001; DH_Z; 1.

PROSITE; PS0001; DH_Z; 1.

PROSITE; PS0001; DH_Z; 1.

PROSITE; PS0002; SH3; 2.

PROSITE; PS002; SH3; 2.

PROSITE; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 SH3 2.
101256 MW; C8FF7681032146B4 CRC64;
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Search completed: September 23, 2002, 09:41:43 Job time: 228 sec

| :|:|| |:|: 862 GRIGWFPSTYVEEEGI 877 77 GVVGYFPRNLVKEQRV 92

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20 VYT- - ISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEM 76

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Gaps

191 357 248

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72 tctggctagtgctcaagaagattataatgccccggactgtagattcattaacgttaaaaa 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         418 CAGTAGCATTGTCCGGGAGGACCTGAACTCGAAACCTGGCAAAATTGATGAAGACCGA 477
                                                                                                                                                                                                                                                                                                                         192 ggctggcagtgtttatggtgatggccaggacgagatgggag---tcgtggggttatttccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 agggcagcagatctatgtgtactcaaagctggtaaaagaaaatggagctggagattttg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         358 GGGAGGCAGTGTTCAGGGAGGTTACTATGGAGACCTGGCAGCCCGCCTGGGCTATTTCCC
                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                        Length 581;
                                                                                                                                                                                                                                        Query Match 19.2%; Score 63.2; DB 1; Length 5 Best Local Similarity 54.3%; Pred. No. 3.6e-11; Matches 175; Conservative 0; Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MELANOMA-INHIBITING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
PRICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
ATTORNEY/AGENT INCORMATION:
NAME: Andrew L. Tiajoloff
REGISTRATION NUMBER: 31,575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18, Application US/08578649
Patent No. 5770366
GENERAL INFORMATION:
APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Buttner
APPLICANT: Brighte Raluza
TITLE OF INVENTION: MELANOMA-INHIBI
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         309 ggatattgacttcttctgcgag 330
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                                                                                sig_peptide
110..178
                                                                                                                                             mat_peptide
179..499
                        CDS
110..499
                  NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                         ; NAME/KEY:
; LOCATION:
US-08-578-649-4
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US-08-578-649-18
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                                                                                                                                                                                                     72 tctggctagtgctcaagaagattataatgccccggactgtagattcattaacgttaaaaa 131
                                                                                                                                                                                                                                                                                                                                        132 agggcagcagatctatgtgtactcaaagctggtaaaagaaaatggagctggagaattttg 191
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م
                                                                                                 Length 459
                                                                                               Score 63.4; DB 1; Length 4
Pred. No. 2.8e-11;
0; Mismatches 101; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08578649
Patent No. 5770366
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Reinhard Buttner
APPLICANT: Reinhard Buttner
APPLICANT: Brigitte Kaluza
TILLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNBER: 20-July-1993
ATTORNEY/AGENT INFORMATION:
NAME: ANGIEW L. Tiajoloff
REGISTRATION UNBER: 31,575
REFERENCE/DOCKET NUMBER: 31,575
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 caggaacttggtcaaggaacage 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            351 CAGTAGCATTGTCCGAGAGGACC 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 1002
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                               Query Match
Best Local Similarity 58.2%;
Matches 153; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 581 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
  mat_peptide
112..432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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: New York
RY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
; NAME/KEY;
; LOCATION:
US-08-578-649-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 2
US-08-578-649-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                      192
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154 tcaaagctggtaaaagaaaatggagctggagaatttgggctggcagtgtttatggtgat 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 tataatgccccggactgtagattcattaacgttaaaaaagggcagcagcagtctatgtgtac 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 aagctctgtgcagatgatgagtgtgtctatactattctctggctagtgctcaagaagat 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .,
o
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 305;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Ulrich Bogdan
APPLICANT: Reinhard Buttner
APPLICANT: Reinhard Buttner
APPLICANT: Brigitte Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                       16.4%; Score 54.2; DB 1; 57.7%; Pred. No. 2.2e-08; Live 0; Mismatches 93;
                                                 NAME: Andrew L. Tiajoloff
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPHAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARATERISTICS:
                                                                                                                                                                                                                                                                                                                                LOCATION: join[1..29, 277..305)
; OTHER INFORMATION: /function= "Primer"
US-08-578-649-8
UMBER: DE P 43 24 247.2
20-July-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 24, Application US/08578649 Patent No. 5770366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
                        FILING DATE: 20-July-199 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                         LENGTH: 305 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 57.7
Matches 139; Conservative
                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 10022
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_RNA
                                                                                                                                                                                                                                                                               MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                linear
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US-08-578-649-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 tcaaagctggtaaaagaaaatggagctggagattttgggctggcagtgtttatggtgat 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214 ggccaggacgagatgggag---tcgtgggttatttccccaggaacttggtcaaggaacag 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 TACTATGGAGATCTGGCTGCTCGCCTGGGCTATTTCCCCAGTAGCATTGTCCGAGAGC 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 aagc¢ctgtgcagatgatgagtgtgtctatactatttctctggctagtgctcaagaagat 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                         91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIE: 10022
COMPUTER FRADABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                     OTHER INFORMATION: /function= "Startcodon Met"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT Ulrich Bogdan
APPLICANT Reinhard Buttner
APPLICANT: Brigitte Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                   Score 57.4; DB 1;
Pred. No. 2.1e-09;
0; Mismatches 91;
     BOER 1035-PFF/ALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-578-649-8
Bquence 8, Application US/08578649
atent No. 5770366
REFERENCE/DOCKET NUMBER: BOEF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 330 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                   17.4%;
nilarity 58.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                        mat_peptide
7..327
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                                                                                                                                                                                                                                                                             misc_RNA
                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 141; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 29
CLASSIFICATION:
                                                                                                                                                                                                                       NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                                                                             NAME/KEY:
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
                                                                                                                                   CUREATION SISTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION DATE: 20-July-1933
ATTORNEY/AGENT INFORMATION:
NAME: Andrew L. Tlajoloff
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LEMGTH: 3565 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: s1g_peptide
LOCATION: 137R
                                                                                                         COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     one-of(2216)
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1586..1719
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2804..2914
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1378..1504
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                    New York
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FEATURE:
NAME/KEY:
LOCATION:
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LOCATION:
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                                     COUNTRY:
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CHER INFORMATION: /note= "N in positions 194, 369
OTHER INFORMATION: and 527 denotes an indefinite number and sequence
THER INFORMATION: of nucleotides "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217 CTATCTCCATGGCCTTCAGGACTACATGCCCCCGACTGCCGATTCCTGACA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 ctatttctctggctagtgctcaagaagattataatgcccggactgtagattcattaacg 124
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..569)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36; Indels
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-U1Y-1993
ATTORNEY/AGENT INFORMATION:
NAME: Andrew L. Tiajoloff
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFANCA: (212) 688-9200
TELEFANCA: (212) 688-9200
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 596 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ulitch Bogdan
APPLICANT: Reinhard Buttner
APPLICANT: Reinhard Buttner
APPLICANT: Brigitte Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSE: Folfe & Lynch
STREET: ,805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 63.3%; Pred. No. 0.00087;
Matches 62; Conservative 0; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-578-649-3
; Sequence 3, Application US/08578649
; Patent No. 57/0366
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      sig_peptide
40..111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    393..503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       549..569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214..347
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40..166
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LOCATION:
FEATURE:
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LOCATION:
LOCATION:
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LOCATION:
FEATURE:
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LOCATION:
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LOCATION:
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LOCATION:
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                                                                                                                                                                                                                                                0; Gaps
OTHER INFORMATION: //note= "N in position 2216
OTHER INFORMATION: denotes an indefinite number ans sequence of
OTHER INFORMATION: nucleotides"
                                                                                                                                                                               Query Match 12.2%; Score 40.4; DB 1; Length 3565; Best Local Similarity 63.3%; Pred. No. 0.002; Matches 62; Conservative 0; Mismatches 36; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 ttaaaaaagggcagcagatctatgtgtactcaaagctg 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
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Source-Sink Relationships and Responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 aatggagctggagaattttggggctggcagtgtttatggtgatggccaggacgagatggga 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204 AATCAAGCCGGAGAAGCAGGGGCCGTCAACGTGCAGGGCGAAATCCAGCAGAAGCTGGAC 263
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Pred. No. 0.19;
0; Mismatches 49; Indels 0
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  THE PHOTOSYNTHESIS RATE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cooley, Michael
APPLICANT: Downley, Bruce
APPLICANT: Gee, Oliver
APPLICANT: The Regents of the University of California
                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,820
FILING DATE: 04-SEP-1997
CLASSIFICATION: 800
PRIOR APPLICATION: B00
PRIOR APPLICATION NUMBER: DE 19502053.7
FILING DATE: 13-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Regulation of Source-Sink Relat
TITLE OF INVENTION: to Stress Conditions in Plants
FILE REFERENCE: 02370-095900US
CURRENT APPLICATION NUMBER: US/09/359,161A
CURRENT FILING DATE: 1999-07-21
                                                                  ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Haley, James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: AGREVO-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-359-161-4/c; Sequence 4, Application US/09359161A; Patent No. 6342656
                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 10.2%;
Best Local Similarity 56.2%;
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1136 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Bradford, Kent J.
APPLICANT: Dahal, Peetambar
APPLICANT: Yang, Hong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                       ZIP: 10020
COMPUTER READABLE FORM:
                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
30..1121
  TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                           CITY: New York
STATE: New York
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N
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                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-860-820-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 7218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                       STALL.
COUNTRY: USA
ZIP: 22313-0299
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM FOC COMPOSTIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
COFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95;
FALKNER, F. G. EDTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 10.3%; Score 34; DB Best Local Similarity 8.1%; Pred. No. 0.33; Matches 19; Conservative 120; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30472/114 IMMU
                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP 91 114 300.6
                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
APPLICATION NUMBER: EP 91 114
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30477
TELECOMMUNICATION INFORMATION:
TELEFRAN: (703)835-9300
TELEFRAN: (703)835-9300
TELEFRAN: (703)835-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08860820 Patent No. 6245967 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Sonnewald, Uwe
APPLICANT: Kossmann, Jens
APPLICANT: Bowlen, Botho
TITLE OF INVENTION: PROCES
                      TITLE OF INVENTION: RECC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
EDNESS: single
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                        1733 AGATCTCCTAGCGAATCAAAAGAAAAAAAGGTTGCTAGGCACCTCTGACCAAGCAGGGT 1674
                                                                                                                                                                                                                                                                                                                                 84 tcaagaagattataatgccccggactgtagattcattaacgttaaaaaagggcagcagat 143
                                                                                                                                                                                                                                                                                                                                                                                                              144 ctatgtgtactcaaagctggtaaaagaaaatggagctggagaatttgggctggcagtgt 203
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                        OTHER INFORMATION: Lycopersicon esculentum plant homolog of yeast; OTHER INFORMATION: SNF1 kinase subunit of protein kinase (LeSNF1) US-09-359-161-4
                                                                                                                                                                                                                                                Score 33.6; DB 4; Length 1929;
Pred. No. 0.24;
0; Mismatches 64; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE.

COUNTRY: USA
2 IP: 2005-3918

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/286,870A
FILING DATE: 05-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSEE: CUSHMAN DARBY & CUSHMAN
SSEE: Intellectual Property Group of
SSEE: PILLSBURY, MADISON & SUTRO LLP
T: 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 70608/220720
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
NFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 05-40G-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/520228
FILING DATE: 09-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8910624.9
FILING DATE: 09-MAY-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BACTERIAL GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/08286870A
Patent No. 6053605
APPLICANT: ELY, S
APPLICANT: TAILOR, RH
APPLICANT: TPAILOR, RH
APPLICANT: TIPPETT, JM
APPLICANT: TIPPETT, JM
APPLICANT: BLENK, RG
ITTLE OF INVENTION: BACTERIAL GENES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                            TYPE: DNA
ORGANISM: Lycopersicon esculentum
                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 52.9%;
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1673 GGAATTTGTTAACAAG 1658
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 1929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 ttatggtgatggccag 219
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ADDRESSEE:
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INFORMATION FOR
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US-08-286-870A-7/c
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COTHER INFORMATION: CDC 1551

OTHER INFORMATION: "n" bases at various positions throughout the sequence

COTHER INFORMATION: represent a, t, c or g

US-09-103-840A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, Oldn C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-220007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.5%; Score 31.2; DB 4; Length 4403765; 47.9%; Pred. No. 34;
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                                                                                                                                                                                                                                                              Length 2159;
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                                                                                                                                                                                                                                                                                                            69;
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                                                                                                                                                                                                                                                              Query Match 10.2%; Score 33.6; DB 3; Best Local Similarity 52.1%; Pred, No. 0.25; Matches 75; Conservative 0; Mismatches 69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1882 TGAAGTTCCAGGCGCCGATGGTGA 1859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, RObert D.
APPLICANT: WHITE, Owen R.
LENGTH: 2159 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
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Matches 90; Conservative
                      TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                            MOLECULE TYPE: CDNA
                                                                                                                                           ; NAME/KEY: CDS
; LOCATION: 1..2159
US-08-286-870A-7
                                                                         linear
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US-09-007-005-17
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                                                                                                                                    ## APPLICANT: FLEISCHMAN, Robert D.

APPLICANT: FRASER, Clair M.

APPLICANT: VEWTER, John C.

TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM

TITLE OF INVENTION: TUBERCULOSIS

FILE REFERENCE: 24366-20007.00

CURRENT FILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PATENTIN VET: 2.1

ELNGTH: 4411529

TYPE: DNA

ORGANISM: Mycobacterium tuberculosis

GTHER INFORMATION: H37RV

US-09-103-840A|1
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Db 426127 cggtgccactgaggatgcctatgtcgacgcttccgctggcgtcgattctggggaacgtaa 426186
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TITLE OF INVENTION: Human and Rat Families of Neuronal Acid-Sensitive
TITLE OF INVENTION: Cationic Channels, Their Cloning and Applications
FILE REFERENCE: 989.5706P
CURRENT APPLICATION NUMBER: US/09/360,197
CURRENT FILING DATE: 1997-07-23
PRIOR APPLICATION NUMBER: 09/129,758
PRIOR FILING DATE: 1998-08-05
PRIOR FILING DATE: 1998-08-05
PRIOR FILING DATE: 1998-08-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 31.2;
Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 13, Application US/09360197 Patent No. 6287859 GENERAL INFORMATION:
APPLICANT: Bassilana, Frederic
                                                                                                Sequence 1, Application US/09103840A
Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 9.5%;
Best Local Similarity 47.9%;
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lazdunski, Michel
APPLICANT: Waldmann, Rainer
APPLICANT: Deweille, Jan R.
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Db 426405 cattgagg 426412
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SOFTWARE: Patentin Ve
SEQ ID NO 13
LENGTH: 1736
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09-360-197-13/c
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; ORGANISM: Hom
US-09-360-197-13
                                                         RESULT 12
US-09-103-840A-1
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                                                                                                                        Gaps
                                             0;
                                                                                                                                                                                                                                                                                                                                                                                GENERAL INPORTATION:
APPLICANT: SZOSTAK, Jack W.
APPLICANT: ROBERTS, Richard W.
APPLICANT: ROBERTS, Richard W.
APPLICANT: ROBERTS, RICHARD W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: PUSIONS
FILE REFERENCE: 07786/350003
CURRENT APPLICATION NUMBER: US/09/007,005B
CURRENT APPLICATION NUMBER: 60/035,963
EARLIER PILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASELSEQ for Windows Version 4.0
LENGTH: 289
    Length 1736;
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                                             Indels
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    DB 4;
Query Match 9.3%; Score 30.8; Di
Best Local Similarity 63.5%; Pred. No. 1.8;
Matches 47; Conservative 0; Mismatches
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Pred. No. 1.1;
96; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (1)...(289)
OTHER INFORMATION: n = A,T,C or
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6.6%; F
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Best Local Similarity
Matches 16; Conserv
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Sequence 1.7 Application US/09244796

Patent No. 6281344

GENERAL INFORMATION:
APPLICANT: Szostak, Jack W.
APPLICANT: Szostak, Jack W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: 199-00-05
FILE REFERENCE: 00786/350007
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1999-01-05
EARLIER PILING DATE: 1999-01-05
EARLIER PILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 9.2%; Score 30.4; DB 4; Length 289; Best Local Similarity 6.6%; Pred. No. 1.1; Matches 16; Conservative 96; Mismatches 130; Indels
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; LCCATION: (1)...(289)
; CTHER INFORMATION: n = A,T,C or G
US-09-244-796-17
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ORGANISM: Artificial Sequence
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aa 268
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Search completed: September 23, 2002, 15:39:48 Job time: 2922 sec

330 6 BD010816 384 6 BD010802 846 9 AF233261 865 9 AF243505 923 6 BD010820	1422 9 HSA242552 330 6 BD010817 384 6 BD010805 929 10 AF243504 947 6 BD010821	958 10 MMUZ43939 1054 10 AF233333 330 6 BD010836 384 6 BD010835	30/ 6 BD010830 261 6 BD010829 484 6 AF233518	23.2 9 HSA23.23.2 21151 9 HS705D16 466 5 AF233519	259 9 HSA252326 545 10 RNU67884 433 6 AX253435 459 6 A42942	459 6 AX216785 459 6 AX255508 459 6 AX287209 459 9 HSMGRPMA	518 9 580 10 580 10 581 6 581 6 442 6 442 6 442 6 3330 6 3330 6 3330 6 3330 6 3330 6 342 8 542 8 543 8 543 8 543 8 543 8 544 8 545 8 545 8 545 8 546 8 547 7 547 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	ZITMAK-ZUUL 29-JUN-2000 JP 2000195911 YASUAKI ITO,KAZUNORI NISHI,KAZUHIRO OGI,SHOICHI OKUBO, PI
330 330 330 330	330 252.2 252.2 252.2 252.2	252.2 252.2 249 249	193.8 190.2 190.2	142	109 67.2 63.4 63.4	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	29 63.4 19.2 30 63.2 19.2 31 63.2 19.2 33 63.4 18.9 33 62.4 18.9 34 62.4 18.9 5. 35 61.8 18.7 5. 36 61.8 18.7 5. 36 61.8 18.7 5. 36 61.8 18.7 5. 41 7.4 40 54.2 17.4 41 54.2 16.4 42 54.2 16.4 44 42 13.4 5. 54.2 16.4 44 42 13.9 5. 44 42 13.4 5. 54.2 16.4 5. 54.2 16.4 5. 54.2 16.4 5. 54.2 16.4 5. 54.2 16.4 5. 54.2 16.4 5. 54.2 16.4 5. 54.2 16.4 5. 54.2 16.4 5. 54.2 16.4 5. 54.2 16.4 5. 54.2 16.4 5. 54.2 16.4 5. 54.2 13.4 14 5. 54.2 13.4 14 5. 56.6 18.9 5. 56.	PD PP PP PP PP PI X
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Robertson, N.G., Heller, S., Lin, J.S., Resendes, B.L., Weremowicz, S., Denis, C.C., Bell, A.M., Hudspeth, A.J. and Morton, C.C.

Direct Submission

Submitted (09-FEB-2000) Pathology, Brigham and Women's Hospital, 75

Francis Street, Boston, MA 02115, USA

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Homo sapiens otoraplin (OTOR) mRNA, complete cds.
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Pred. No. 3.1e-88;
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/db_xref="taxon:9606"
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Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,

Yoshimura,K. and Tanaka,H.

Novel polypeptide and Dha thereof

Patent: JP 201069994-A 3 21-MAR-2001;

TAKEDA CHEMICAL INDUSTRIES LTD
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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PRI 06-JUL-2000

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NLVKEQRVYQEATKEVPTTDIDFFCE"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Yoshimura,K. and Tanaka,H.
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Patent: JP 2001069994-A 21 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
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PN JP 2001069994-A/21
PD 21-MAR-2001
PF 29-JUN-2000 JP 2000195911
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100.0%; Pred. No. 3.4e-88;
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/db_xref="taxon:9606"
/chromosome="20"
/map="20p11"
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                                                                                                                                                        /codon_star.-.
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SAQEDYNAPDCRFINVKKGONYVSKLVKENGAGEFWAGSVYGDGQDEMGVVGYFPR
NLVKEQRYVQEATKEVPTDIDFFCE"

NLVKEQRYVQEATKEVPTDIDFFCE"
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Cohen-Salmon,M., Frenz,D., Liu,W., Verpy,E., Voegeling,S. and
Petit,C.
Fdp, a New Fibrocyte-derived Protein Related to MIA/CD-RAP, Has an
in Vitro Effect on the Early Differentiation of the Inner Ear
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Cohen-Salmon,M., Frenz,D., Verpy,E., Voegeling,S. and Petit,C.
Direct Submission
Submitted (09-MAR-2000) Biotechnologies, Institut Pasteur, 25 rue
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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10998416
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illarity 100.0%; Pred. No. 3.4e-88;
Conservative 0; Mismatches 0;
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1. 846
/gene="foto"
45. 431
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/gene="MIAL"
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Genetics, Institute of Medical Biochemistry and Genetics, Blegdamsvej 3, 2200 Copenhagen N, DENMARK evised by author 02 AnG-1999 Related sequence: AJ243939 (Mus musculus mRNA) Related sequences: AJ253124 to AJ252327 (genomic sequence).
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                                                                                                                                                                                                                                   /chromosome="20"
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100.0%; Score 330; DB 9;
Best Local Similarity 100.0%; Pred. No. 3.7e-88;
Matches 330; Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
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/gene="MIAL"
/number=3
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/gene="MIAL"
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Homo sapiens mRNA for melanoma inhibitory activity like protein
                                                                                                                            C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1422)

Rendtorff, N.D., Frodin, M., Attie-Bitach, T., Vekemans, M. and
                                                  YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA
C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P9/00,A61P19/02,
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Submitted (21-MAY-1999) Rendtorff N.D., Department of Medical
  YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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C12P21/08,C12N15/00,A61K37/02,C12N5/00
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Location/Qualifiers
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/db_xref="taxon:9606"
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Rendtorff, N.D.
  PI YASUAKI I
SHINICHI MOGI,
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CIZN15/09,A61K38/00,A61K48/00,A61P9/00,A61P19/02,
A61P19/08,
                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; I (bases 1 to 384)
Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y., Yoshimura,K. and Tanaka,H. thereof Patent: JP 2001069994-A 6 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
     ggagaattttgggctggcagtgtttatggtgatggccaggacgagatgggagtcgtgggt 240
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                                                                          115 TATACTATTTCTCTGGCAAGAGCACAGGAAGATTACAATGCCCCAGACTGTAGGTTCATC 174
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                                 GGAGAGTTTTGGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGATGGGAATTGTAGGT
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9
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llarity 85.4%; Pred. No. 6.7e-65;
Conservative 0; Mismatches 48;
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                                                                                                                                                                                                                   DNA
                                                                                                                                                                                                             384 bp
Novel polypeptide and DNA thereof.
BD010805.1 GI:18639178
JP 2001069994-A/6.
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sp. (mouse)'.
                                                                                                                  1 .384
/organism="Mus sp."
/db_xref="taxon:10095"
68 c 111 g
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JP 2001069994-A/6
21-MAR-2001
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PI YUKO NOGUO
PC C12N15/09
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PI YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA
PC | C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P9/00,A61P19/02, PC
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Novel polypeptide and DNA thereof
Patent: JP 2011069994-A 18 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
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/organism='Mus sp. (mouse)'.
Location/Qualifiers
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Pred. No. 6.6e-65;
0; Mismatches 48
                                                                                                                                                                                                                                             DNA
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/db_xref="taxon:10095"
60 c 92 g
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JP 2001069994-A/18 ·
21-MAR-2001
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JP 2001069994-A/18.
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85.4%;
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289
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                                                                              /db_xref="taxon:10095"
158 c 221 g
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JP 2001069994-A/22
21-MAR-2001
29-JUN-2000 JP 2000195911
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/organism="Mus sp."
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Best Local Similarity 85.4%;
Matches 281; Conservative (
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PN JP 2001069
PD 21-MAR-200
PF 29-JUN-200
PR YASUAKI IT
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G01N33/53/,
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RAGEDYNAPDCRFIDVKKGQQIYVYSKLVTENGAGEFWAGSVYGDHQDEMGIVGYFPS
NLVKEQRYVQEATKEIPTTDIEG
1 156 c 293 g 293 L
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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 294
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Cohen-Salmon,M., Frenz,D., Liu,W., Verpy,E., Voegeling,S. and Petit,C.
Fdp, a New Fibrocyte-derived Protein Related to MIA/CD-RAP, Ha Mesenchyme
Mesenchyme
J. Biol. Chem. 275 (51), 40036-40041 (2000)
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2 (bases 1 to 929)
2 (bases 1 to 929)
Cohen-Salmon,M., Frenz,D., Verpy,E., Voegeling,S. and Petit,C. Direct Submission
Submitted (09-MAR-2000) Biotechnologies, Institut Pasteur, 25
du Dr. Roux, Paris 75015, France
Location/Qualifiers
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                     235 GGAGAGTTTTGGGCTGGCAGTGTTTATGGTGACCACCAGGATGAGATGGGAATTGTAGGT
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/protein_id="AAG42355.1"
/db_xref="G1:11991842"
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Pred. No. 7.6e-65;
0; Mismatches 48;

    929
    organism="Mus musculus"

                                                                   /strain="BALB/c"
/db_xref="taxon:10090"
/chromosome="2"
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9. 30c
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Similarity 85.4%;
31; Conservative (
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/gene="Fdp"
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house mouse.
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Best Local S:
Matches 281,
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PAT 31-JAN-2002
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C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P9/00,A61P19/02, PC
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                                                                                                                         Eukarypta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I toases 1 to 947.
Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y., Yoshimura,R. and Tanaka,H.
Yoshimura,R. and Tanaka,H.
Patent: JP 2001069994-A 22 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                               C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50,
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linear
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Pred. No. 7.6e-65;
0; Mismatches 48
DNA
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(bases 1 to 1054)

Robertson, M. G., Heller, S., Lin, J.S., Resendes, B.L., Weremowicz, S., Denis, C.S., Bell, A.M., Hudspeth, A.J. and Morton, C.C.

Direct Submission
Submitted (10-FEB-2000) Pathology, Brigham and Women's Hospital, 75
Francis Street, Boston, MA 02115, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation-"MARILILLLGGLVVLCAGHGVFMDKLSSKKLCADEECVYTISLA
RAQEDYNAPDCRFIDVKKGQQIYVYSKLVTENGAGEFWAGSVYGDHQDEMGIVGYFPS
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Robertson, N.G., Heller, S., Lin, J.S., Resendes, B.L., Weremowicz, S., Denis, C.S., Bell, A.M., Hudspeth, A.J. and Morton, C.C.
A Novel Conserved Cochlear Gene, OTOR: Identification, Expression Analysis, and Chromosomal Mapping Genomics 66 (3), 242-248 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                121 aacgttaaaaaagggcagcagatctatgtgtactcaaagctggtaaaagaaaatggagct 180
                                                                                                                                     241 tatttccccaggaacttggtcaaggaacagcgtgtgtaccaggaagctaccaaggaagtt 300
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                318 TATTTCCCCAGCAACTTGGTGAAGGAGCAGCGTGTATACCAGGAGGCCCACCAAGGAGATC 377
                                                                                  198 GATGTCAAGAAAGGGCAGCAGCAGCTGTTTACTCCAAGCTGGTAACAGAAAACGGAGCT
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llarity 85.4%; Pred. No. 7.8e-65;
Conservative 0; Mismatches 48;
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/product="otoraplin"
/protein_id="AAF82079.1"
/db_xref="GI:8927430"
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/db_xref="taxon:10090"
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Identification and Characterization of an Inner Ear-Expressed Human Melanoma Inhibitory Activity (MIA)-like Gene (MIAL) with a Frequent Polymorphism That Abolishes Translation Genomics 71 (1), 40-52 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="marilililigglvvicagHgvFmDKLSSKKLCADEECvYTISLA
RAQEDYNAPDCRFIDVKKGQQIYVYSKLVTENGAGEFWAGSVYGDHQDEMGIVGYFPS
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                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 958)
                                                                                                                                                                                                       Mus musculus mRNA for melanoma inhibitory activity-like protein (Mial gene).
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                  305 TATTTCCCCACCAACTTGGTGAAGGAGCAGCTGTATACCAGGAGCCACCAAGGAGATC 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (20-JUL-1999) Rendtorff N.D., Department of Medical Genetics, Institute of Medical Biochemistry and Genetics, Blegdamsvej 3, 2200 Copenhagen N, DENMARK Related sequence: Al242552.

Location/Qualifiers
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/protein_id="CAC27444.1"
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                                                                                                                                                                                                                                                   AJ243939.1 GI:12619174 melanoma inhibitory activity-like protein; Mial gene. house mouse.
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Pred. No. 7.7e-65;
0; Mismatches 48;
                                                                                                                                                                                              mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="2"
/map="79.4-80 cm"
/tissue_type="whole fetus"
/de_stage="12.5 pc"
/gene="Mial"
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                                                                  301 cccaccacgatattgacttcttctgcga 329
                                                                                  365 CCAACCACGATATTGACTTCTTCTGTGA 393
                                                                                                                                                                                            958 bp
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85.4%;
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Rendtorff, N.D.
Direct Submission
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Best Local Similarity 85.4
Matches 281; Conservative
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ROD 06-JUL-2000

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AUTHORS
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Edatus Sp.
Manmalla; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P9/00,A61P19/02,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, G01N33/53//
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                                                                                                          241 tatttccccaggaacttggtcaaggaacagcgtgtgtaccaggaagctaccaaggaagtt 300
                                                                                                                     132 TATACTATTTCTCTGGCAAGAGCACAGGAAGATTACAATGCCCCAGACTGTAGGTTCATC 191
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                                                                Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,
Yoshimura,K. and Tanaka,H.
Novel polypeptide and DNA thereof
Patent: JP 2001069994-A 37 21-WAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
OS Rattus Sp. (rat)
PN JP 2001069994-A/37
PD 21-MAR-2001
PF 29-JUN-2000 JP 2000195911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 6; Length 330;
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                                                                                                                                                                                                                                DNA
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Pred. No. 6e-64;
0; Mismatches
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Location/Qualifiers
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/db_xref="taxon:10118"
62 c 91 g
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JP 2001069994-A/37.
Rattus sp.
Rattus sp.
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PN JP 20010699
PD 21-MAR-2001
PR 29-JUN-2000
PR YASUAKI ITC
PI YUKO NOGIC;
PC CIINIS/09,A
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es 279; Conserv
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Best Local Si
Matches 279;
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PAT 31-JAN-2002
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C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P9/00,A61P19/02, PC
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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: C07K14/47,C07K16/18,C12N1/21,C12N5/10,G01N33/15,G01N33/50,
YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI
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Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,

Yoshimura,K. and Tanaka,H.

Novel Polypeptide and DNA thereof

Patent: JP 201069994-A 36 21-MAR-2001;

TAKEDA CHEMICAL INDUSTRIES LTD
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1. .384
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Location/Qualifiers
1. .384
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JP 2001069994-A/36.
                                                                            /organism="Rattus sp."
/db_xref="taxon:10118"
72 c 109 g
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JP 2001069994-A/36
21-MAR-2001
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Search completed: September 23, 2002, 14:58:47 Job time: 2061 sec
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C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P9/00,A61P19/02, PC
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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121 aacgttaaaaaagggcagcagatctatgtgtactcaaagctggtaaaagaaaatggagct 180
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Yoshimura,K. and Tanaka,H.
Novel polypeptide and DNA thereof
Novel polypeptide and DNA thereof
TAKEDA CHEMICAL INDUSTRIES LTD
OS Rattus Sp. (rat)
NN JP 20010659914-A/31
PN JP 20010659914-A/31
PN JP 20010659914-A/31
PN JP 20-JUN-2000 JP 2001195911
PR YASUARI ITO,KAZUNORI NISHI,KAZUHIRO OGI,SHOICHI OKUBO,
SHINICHI MOGI,
PT YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA
PC CINNIS/09,A61K38/00,A61K45/00,A61K48/00,A61P9/00,A61P19
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/organism="Rattus sp."
/db_xref="taxon:10118"
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JP 2001069994-A/31.
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61.6 18.7 465 9 AA003262 61.6 18.7 555 10 B1851688 61.4 18.6 698 19 A6220915 61.2 18.5 452 9 AA627297 60.2 18.2 453 9 AA627297 60.2 18.2 409 9 AA644509 58.8 17.8 496 9 AA644509 56.4 17.1 425 10 W75984 56.4 17.1 476 9 AA644509 56.4 17.1 476 9 AA644509 56.4 17.1 476 9 AA644509 56.4 17.1 476 9 AA692842 56.4 17.1 475 9 AA692842 55.2 16.7 481 9 A172559 55.2 16.4 437 9 AA7566 53.4 16.2 391 0 W4756 53.4 16.2 392 10 W4756 53.4 16.2 392 10 W4756 53.4 16.2 392 10 W4756 53.4 16.2 392 10 W4756 53.5 16.1 468 9 AA5977676 52.6 15.9 589 9 AV169321 52.2 15.8 668 10 W44019 52.2 15.8 668 10 W44019	ALIGNMENTS BB611549 BB611549 BB611549 RIKEN full-length enriched, 13 days embryo head Musmusculus cDNA clone 3110083012 5', mRNA sequence. BB611549.1 GI:15393547 BB611549.1 GI:15393547 BB611549.1 GI:15393547 EST. Wus musculus ENAMMANIA: Entheria: Rodentia: Sciurognathi: Muridae: Mus. Wusmusculus Eukaryota: Metazoa; Chordata; Craniata: Vertebrata: Euteleostomi; Bukaryota: Metazoa; Chordata; Craniata: Vertebrata: Euteleostomi; Bukaryota: Metazoa; Chordata; Craniata: Vertebrata: Euteleostomi; Arakawa-T., Carninoi,P., Fukuda.S., Furuno,M., Hanagaki,T., Hara.A. Hiramoto,K., Hori,F., Ishi,Y., Ito,M., Kawai,J., Konno,H., Sasaki M., Koyais., Matsuyama,T., Milzaki,T., Sogabe,Y., Suzuki,H., D., Shibatas, T., Sakaic,R., Shiraki,T., Sogabe,Y., Suzuki,H., BIKEN Mouse ESTS (Arakawa,T., et al. 2001) Contact: Yookhihide Hayashizaki Contact: Yookhihide Hayashizaki Contact: Yookhihide Hayashizaki The Institute of Physical and Chemical Research (RIKEN) Tel: B1-45-503-922 Fax: B1-45-503-
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 BB611549 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT
<pre>4.5 Compugen Ltd. ; Search time 1903.73 Seconds (without alignments) 2339.615 Million cell updates/secatattgacttcttctggag 330atattgacttcttctggag 330 sidues ters: 27472414</pre>	results predicted by chance to have a lite the total score distribution. SUMMARIES Description Description BEL36443 AW02334 AW02334 AW02334 AW02334 AW02334 AW02344 BEG36443 BEG36443 AW02344 AW02344 BEG47928 BA22797 B1492218 W74647 B149218 W74647 B1492218 B1492218 B1492318 B1493750 B149350 B1333423 A1323423 A1323423 A1323423 A1323423 A1323423
GenCore version 4. Copyright (c) 1993 - 2000 Co cleic search, using sw model September 23, 2002, 13:38:35; US-10-019-455A-23 330 1 catggaatatttatggaccg IDENTITY_NUC Gapop 10.0, Gapext 1.0 13736207 seqs, 6748477542 resi hits satisfying chosen paramete length: 0 length: 2000000000 : Minimum Match 0% Maximum Match 100% Listing first 45 summaries	EST:* 1: em_estba:* 2: em_estha:* 3: em_estha:* 5: em_estho:* 6: em_estor:* 6: em_estor:* 6: em_estro:* 8: em_estro:* 10: 9b_est1:* 10: 9b_htc:* 11: 9b_htc:* 11: 9b_htc:* 12: 9b_est2:* 11: 9b_htc:* 13: em_gss_lnu:* 14: em_gss_lnu:* 15: em_gss_lnu:* 16: em_gss_lnu:* 16: em_gss_lnu:* 16: em_gss_lnu:* 16: em_gss_lnu:* 18: em_gss_lnu:* 19: 9b_est2:* 10: 9b_est1:* 10: 9b_est2:* 11: 9b_htc:* 11: 9b_htc:* 12: 9b_est2:* 13: em_estro:* 14: em_gss_lnu:* 15: em_gss_lnu:* 16: em_gss_lnu:* 16: em_gss_lnu:* 16: em_gss_lnu:* 17: 9b_est2:* 18: em_gss_lnu:* 18: 9b_est2:*
OM nucleic - nuc Run on: Title: Perfect score: Sequence: Scoring table: Scoring table: Al number of Minimum DB seq Maximum DB seq Maximum DB seq Maximum DB seq	Pred. No. score greand is default No. Score greand is default No. Score Greand is 157.4 4 131.6 5 100.4 2 130.4 5 110 6 3.4 4 131.6 5 10 6 3.4 5 10 6 3.4 5 10 6 3.4 5 10 6 3.4 5 10 6 3.4 5 10 6 3.4 5 10 6 3.4 5 10 6 3.4 5 10 6 3.4 5 10 6 3.4 5 10 6 3.4 5 10 6 3.4 5 10 6 3.4 5 10 6 3.4 5 10 6 10 6 3.4 5 10 6 10 6 3.4 5 10 6 10 6 10 6 10 6 10 6 10 6 10 6 10

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AUTHORS
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                                                                                                                                                                                                   encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Yamanaka, I., Kiyoswa, H., Kondo, S., Saito, T., Shinagawa, A., Aizawa i.K., Fukuda, S., Hara, A., Itch, M., Kawai, J., Shibata, K., Arakawa, T., Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Func. Genomics 2 pre, L72-L86 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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                                                                                                          Carninci, P., Sugahara
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                               sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Site_1: XhoI; Site_2: SstI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib-"RIKEN full-length enriched, 13 days embryo head"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          317
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RIKEN integrated sequence analysis (RISA) system--384-format
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Pred. No. 3.1e-62;
0; Mismatches 48; Indels 0
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/dev_stage="13 days embryo"
/lab_host="SOLR"
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/db_xref="taxon:10090"
/clone="3110083012"
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1. .696
                                                                                                                                   Y. and Hayashizaki, Y.
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Best Local Similarity 85.4%;
Matches 281; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e mouse tissues.
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ORIGIN
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Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the .minscore 18 and .minmatch 12 options.
25-APR-2001
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1 (bases 1 to 57)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Keele, J.W.
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                                                                                                                                                                                                                                                                                                                                                                           Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001) 21180013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"Vector: pCMV SPORT6; Site_1: xbaI; Site_2: xhoI; Library made from pooled tissue from day 20 and day 40
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  EST
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BE236443 1near 527 bp mRNA linear 144645 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TTEL: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 190.4; DB 9;
Pred. No. 2e-44;
0; Mismatches 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9913"
/clone_lib="MARC 4BOV"
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Seq primer: ATTTAGGTGACACTATAG.
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/lab_host="DH10B"
/note="Vector: pCMV SF
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78.28;
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94 c
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ORIGIN
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VERSION
                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
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AUTHORS
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="InAGE:2487192"
/clone=lib="Morton Fetal Cochlea"
/tissue_type="cochlea"
/tasue_type="cochlea"
/dev_stage="l6-22 week fetus"
/dab_host="SOLR cells (kanamycin resistant)"
/dab_host="Corganisms cells (kanamycin resistant)"
/dap_host="Corganisms cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 349)
Robertson,N.G., Khetarpal,U., Gutierrez-Espeleta,G.A., Bieber,F.R. and Morton,C.C. Isolation of novel and known genes from a human fetal cochlear cDNA library using subtractive hybridization and differential screening denomics 23, 42-50 (1994)
                                                                                                                                                                                                                                                  AW023324 349 bp mRNA linear EST 13-SEP-1999 df53d01.yl Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:2487192 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Morton, C. C.
Departments of Pathology and Obstetrics, Gynecology and
Reproductive Biology
Brigham and Women's Hospital
75 Francis Street, Harvard Medical School, Boston, MA 02115, USA
77137 9860
Email: Comortonebics.bwh.harvard.edu
Email: ccmortonebics.bwh.harvard.edu
Email: ccmortonebics.bwh.harvard.edu
67 Health Intramural Sequencing Center (NISC; see
http://www.nisc.nih.gov).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Plate: LLAMGIB9 row: G column: 1 Seq primer: M13RP1 reverse primer (ABI).

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     293 TATTTTCCCAGCAACTTGGTCCAGGAACAACATGTGTACCAAGAAGCCACCAAGGAAGTT 352
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Pred. No. 5.9e-35;
0; Mismatches 1;
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                                                       301 cccaccacggatattgacttcttctgcgag 330
                                                                                      353 CCTACCACGGATATTGACTTTTTCTGCGAG 382
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illarity 99.4%;
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AW021345 318 bp mRNA linear EST 13-SEP-1999 df21c01.yl Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE2484072 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolation of novel and known genes from a human fetal cochlear CDNN library using subtractive hybridization and differential screening Genomics 23, 42-50 (1994)
                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 338)
Robertson, N.G., Khetarpal, U., Gutierrez-Espeleta, G.A., Bieber, F.R. and Morton, C.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: ccmorton@bics.bwh.harvard.edu
Dans sequencing and analyses were performed by National Institutes
of Health Intramural Sequencing Center (NISC; see
http://www.nisc.nih.gov).
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Plate: LLAM6181 row: E column: 1
                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reproductive Biology
Brigham and Women's Hospital
Foracis Street, Harvard Medical School, Boston, MA 02115, USA
Tel: 617 732 7980
Fax: 617 738 6996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Morton, C. C. Departments of Pathology and Obstetrics, Gynecology and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2484(D72"
/clone_lib="Morton Fetal Cochlea"
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
                                                                                                                                                                                                                       AW021345.1 GI:5874805
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Best Local Similarity 97.1%;
Matches 134; Conservative
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148 c
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Matches 122; Conservative
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (basea 1 to 678)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
'Hiramoto,K., Hori,F., Ishli,Y., Ito,M., Kawai,J., Konno,H., Kouda
'M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
'D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTS (Arakawa,T., et al. 2001)
Upublished (2001)
Contact: Voshinide Hayashizaki,Y.
In Inboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara , Y. and Hayashizaki, Y. Computer-based methods for the mouse full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                 BB647928 RIKEN full-length enriched, 16 days embryo head Mus musculus cDNA clone C130025A07 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
'M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare [Lil-length cDNA libraries for rapped discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
'S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="head"
/dev_stage="16 days embryo"
/lab_host="DH10B"
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/strain="C57BL/6J"
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/clone="C130025A07"
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121 ATTGACTTCTTCTGCGAG 138
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prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5 with the primer adapter of sequence [7] was prepared with the was cloned to the xNoT and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA222797 492 bp mRNA linear EST 18-FEB-1997 mv77b12.r1 Soares mouse 3NME12 5 Mus musculus cDNA clone IMAGE:661055 5', mRNA sequence.
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse Lissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGCATCCAAGAGCTCTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 atactatttctctggctagtgctcaagaagattataatgccccggactgtagattcatta 121
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Contact: Marra M/Mouse EST Project
Washugton University School of MedicineP
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.3%; Score 110; DB 9; Length 67
85.9%; Pred. No. 3.8e-21;
iive 0; Mismatches 20; Indels
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High quality sequence stop: 440.
Location/Qualifiers
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/db_xref="taxon:10090"
/clone="IMAGE:661055"
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w74647 533 bp mRNA linear EST 17-OCT-1996 zd77e05.s1 Soares_fetal_heart_NDHH19W Homo sapiens cDNA clone IMAGE:346688 3' similar to PIR:540238 S40238 melanoma-derived protein MIA - human ;, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 673 Std Error: 0.00
Seq primer: ETPPIMER
High quality sequence stop: 403.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 576;
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/db_xref="GDB:1272063"
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Best Local Similarity 100.0
Matches 82; Conservative
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Isolation of novel and known genes from a human fetal cochlear cDNA
library using subtractive hybridization and differential screening
Genomics 23, 42-50 (1994)
                                                                                                                                                                         BI492218 576 bp mRNA linear EST 28-AUG-2001
df21c01.w1 Morton Fetal Cochlea Homo sapiens cDNA clone
IMAGE:2484072 3', mRNA sequence.
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Mammalia; Eutherla; Primates; Câtarrhini; Hominidae; Homo.
1 (Nases 1 to 576)
Robertson.N.G., Khetarpal.U., Gutierrez-Espeleta,G.A., Bieber,F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ccmorton@bics.bwh.harvard.edu
DNA sequencing and analyses were performed by National Institutes
of Health Intramural Sequencing Center (NISC; see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95130111
Contact: Morton, C. C.
Departments of Pathology and Obstetrics, Gynecology and
Reproductive Biology
Brigham and Women's Hospital
Pris 617 732 7980
Pax: 617 738 6996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.nisc.nih.gov).
This clone is available royalty-free through LLNL; contact the This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Plate: LLAM6181 row: E column: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194 ctggcagtgtttatggtgatggccaggacgagatgggagtcgtgggttatttccccagga 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CTGGCAGTGTTATATGGTGACCACCAGGATGAGATGGGAATTGTAGGTTATTTCCCCAGCA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       constructed by Bento Soares and M. Fatima Bonaldo. 96 c 111\ g 144\ t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.5%; Score 107.2; DB 9; Length 492; 86.8%; Pred. No. 2.2e-20; Live 0; Mismatches 18; Indels 0;
                       /clone_lib="Soares mouse 3NME12
/sex="unknown"
                                                                                                                 /dev_stage="12.5dpc total fetus"
/lab_host="DH10B"
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                                                                                   /tissue_type="fetus"
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Homo sapiens

ORGANISM

RENCE UTHORS MEDLINE COMMENT

FEATURES

JOURNAL

TITLE

human.

BI492218

ACCESSION VERSION KEYWORDS

LOCUS BI492218/c

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source
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DEFINITION
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ORIGIN
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TITLE
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BF691795
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ArCC/DCTD/DTP
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Theyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Phtp://image.llnl.gov.h. column: 12
                                                                                                                                                                                                                                                                                                                                                   72 tctggctagtgctcaagaagattataatgccccggactgtagattcattaacgttaaaaa 131
                                                                                                                                                                                                                                                                                                                          327 CATGGCTGTGGCCCTTCAGGACTACATGGCCCCCGACTGCCGATTCCTGACCATTCACCG 268
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                                                                                                                                                                                      Score 64.6; DB 10; Length 533;
Pred. No. 4.5e-08;
0; Mismatches 99; Indels 10;
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/db_xref="taxon.9606"
/clone="IMAGE:4333499"
/clone_Ib="NIH_MGC_62"
/tissue_type="melanotic melanoma, high MDR"
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Location/Qualifiers
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58.6%;
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Matches 154;
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                                                                                                                                   BASE COUNT
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BF691795
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//incle="Organ: Skin: Vector: pDNR-LLB (Clontech); Site_1: Sfil (ggccgctcggcc); Site_2: Sfil (ggccattaggcc); Double-stranded CDNA was prepared from cell line RNA. 5' adaptors were used in cloning as follows: 5' adaptors sequence: 5'-CACGGCCATATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGAGGCGCACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 890)
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Tissue Procurement: ATC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC.clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Location/Qualifiers
Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          166 CATGGCTGTGGCCCTTCAGGACTACATGGCCCCCGACTGCCGATTCCTGACCATTCACG
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/lab_host="DH10B (Tl phage-resistant)"
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58.2%; Pred. No. 8.8e-08;
iive 0; Mismatches 101;
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BG766328
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Best Local Similarity
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/clone_lib="NIH_MGC_49"
/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally cloned
into Ecori/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-CDNA synthesis kit (stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, T=1:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AG141467 657 bp DNA linear GSS 08-JAN-2002
Pan troglodytes DNA, clone: RP43-001J02.T7, genomic survey
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GSS; GSS (genome survey sequence).
Ban troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee
Male BAC Library clone:RP43-001J02.T7.
Pan troglodytes
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 tctggctagtgctcaagaagattataatgcccggactgtagattcattaacgttaaaaa 131
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Frliyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
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BAC end sequences of Library RPCI-43
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Pred. No. 1.4e-07;
0; Mismatches 101;
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58.2%;
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336 c
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Matches 153; Conservative
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AG141467/c
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/clone_lib="NIH_MGC_49"
/tissue_type="melanotic melanoma, high MDR (cell line)"
/lab_host="DH10B (phage-resistant)" is the corporate skin; Vector: pOTB7; Site_1: XhoI; Site_2: Anote="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2: ECORI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(6). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript IRT (Life Technologies). Note: this is a NIH_MGC
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602739414F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4869267 5',
mRNA sequence.
BG765502
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo
1 | (bases 1 to 1140)
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: ArCC/DCTD/DTP
Tissue Procurement: ArCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMIATO row: 1 column: 04
High quality sequence stop: 509.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Pred. No. 1.2e-07;
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/db_xref="taxon:9606"
/clone="IMAGE:4869267"
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ilarity 58.2%;
Conservative
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Matches 153; Conserv
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In unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CSPR clone distribution information can be
infoelmage-lln.gov

Seq primer: -400P from Gibco.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aju op mRNA linear EST 29-NOV-2000 nadl3c10.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3365371 3 similar to SW:MIA_HUMAN Q16674 MELANOMA DERIVED GROWTH REGULATORY PROTEIN PRECURSOR; mRNA sequence.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: lung, Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_Lu5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 430)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                              /clone_lib="RPCI-43 Chimpanzee Male BAC Library"
143 c 117 g 189 t 7 others
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                                                                                                                                                                                                                                                                             657;
                                                                                                                                                                                                                                                                             Length
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Pred. No. 2.1e-07;
                                                                      1. .657
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-001J02.17"
                                                                                                                                                                                                                                                                                                             0; Mismatches
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/lab_host="DH10B"
                                                                                                                                                /sex="male"
/cell_type="lymphocytes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                     Location/Qualifiers
: pBACe3.6
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                    ECORI
                                    : ECORI
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R.Site 2
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Best Local Similarity
Matches 63; Conserv
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BF439750/c
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AUTHORS
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                                                     FEATURES
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1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo. " 124\ c 125\ g 81\ t
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                                                                                                                                                                                                            3
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 442)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Insert Length: 1148 Std Error: 0.00
Seq primer: -41m13 fwd. Err from Amersham
High quality sequence stop: 337.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                             388 rargcccaagcregcreacegaagcrererecegaceageagrecagecaccrarcre 329
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                                                                                                                                                   Score 61.8; DB 10;
Pred. No. 2.7e-07;
0; Mismatches 102;
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/clone_lib="NCI_CGAP_GCB1"
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/db_xref="taxon:9606"
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                                                                                                                                                      Query Match 18.7%;
Best Local Similarity 57.8%;
Matches 152; Conservative
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]. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT713 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

| [bases 1 to 388]
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicqap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicqap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BE625492 and linear EST 24-AUG-2Cul9d01.yl Soares_mammary_gland_NMLMG Mus musculus cDNA clone IMAGE:3372385 5' similar to SW:MIA_MOUSE Q61865 MELANOMA DERIVED GROWTH REGULATORY PROTEIN PRECURSOR; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumor Gene Index (1997)
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                      191
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/clone="IMAGE:3372385"
/clone_lib="Soares_mammary_gland_NMLMG"
                                                                                                                                                                         Ouery Match
Best Local Similarity 57.8%; Pred. No. 2.7e-07;
Matches 152; Conservative 0; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="female (lactating)"
/tissue_type="mammary gland"
/lab_host="DH108"
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Seq primer: -40RP from Gibco
High quality sequence stop: 382.
Location/Qualifiers
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I and cloned into the Not I and Eco RI sites of the modified pYT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo." 105 c 110 g 93 t
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Pred. No. 3e-07;
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54.0%;
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Melanoma inhibitor
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                                                               Recombinant human
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                                                                                                                                                                                                                                                                                                   Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human MLP nucleotide sequence SEQ ID NO:23
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                                                                                            AAD18732
AAQ84052
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AAH99775
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WPI; 2001-159271/16.
P-PSDB; AAB69126.
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Mouse MLP nucleoti
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N. Ganesag_05282:*
N. Ganesag_05282:*
SIDSI/gcgdata/genesag/genesegn-embl/NA1980.DAT:*
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SIDSI/gcgdata/geneseg/genesegn-embl/NA1982.DAT:*
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/SIDS1/gogdata/geneseg/genesegn-embl/NA2001B.DAT:
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                                                                                                                                                                                                               3472872
           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                                                                                                                                         1736436 seqs, 858457221 residues
                                                                         September 23, 2002, 15:36:31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                    nucleic search, using sw model
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AAS17583
AAH26341
AAH98228
AAH26342
AAF59083
AAH26343
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AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
          Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and joint
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ive 0; Mismatches 0;
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                                                                                                                                                                                                                       in the exemplification of the present invention.
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The present invention describes novel MLP proteins and their encoding DNAS. The MLP proteins and DNAS have antiinflammatory and cardiant activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAS can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic anglogenesis.

AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
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                                           Ogi K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nseq
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                                                                                                                                                                                                                                                                                                                                  Smith RF, Xiang 2;
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                                                                                /*tag= a
/product= "Human secreted protein"
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100.0%; Pred. No. 3.1e-97;
ive 0; Mismatches 0;
                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 44; 92pp; English.
                                                                                                                                                                                                                                2000US-196603P.
2000US-199417P.
                                                                                                                                                                                                 11-APR-2001; 2001WO-US11797.
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24-APR-2000;
               Homo sapiens
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Isolated human growth regulatory-like polypeptide useful for treating e.g. Alzheimer's disease, cancer, autoimmune disorders, hyperproliferative disorders, coagulation disorders, and nervous system
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cartilage development and maintenance, inhibition of melanoma cell growth and tumours, including neuroectodermal tumours such as gliomas. The polynucleotides can also be used to design probes
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neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;
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301 cccaccacggatattgacttcttctgcgag 330
                                                               Example 1; Page 114; 119pp; English.
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Isolated human growth regulatory-like polypeptide useful for treating e.g. Alzheimer's disease, cancer, autoimmune disorders, hyperproliferative disorders, coagulation disorders, and nervous system
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                                                                                                                                                                                                                                                                                  urchin and tomato. These were derived from expressed sequence ta from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess blodiversity and for nutritional purposes. The present sequence
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diagnosis;
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                                                                                               100.0%; Score 330; DB 22;
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ive 0; Mismatches 0;
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nes 330; Conser
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tomatc; monkey; dog; sea urchin; expressed sequence tag; EST;
diagnostics; forensic test; gene mapping; genetic disorder;
blodiversity; gene therapy; nutrition; ss.
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Zhang J, Werhman T;
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                                                                                                                                                            The present sequence is that of a novel nucleic acid that was assembled from human thymus CDNA library-derived Hyseq clone identification number 1637277 (see AAH26341). A recursive algorithm was used to extend the clone by pulling additional sequences from different databases. A full-length sequence (see AAH26343) encoding novel human growth regulatory-like polypeptide (GRLP, see AAB82671) was subsequently obtained. Human GRLP belongs to the same protein family as growth regulatory protein procursor (64% similarity and 45% identity over 111 amino acids) or melanoma inhibitory activity, cattle cartilage-derived retinoic acid sensitive protein (CD-RAP, 44% identity and 64% similarity over 126 amino acids) and other retinoic acid sensitive protein (CD-RAP, 44% identity and 64% similarity over 126 amino acids) and other retinoic acid sensitive protein (CD-RAP, 44% identity and 64% similarity over 126 amino acids) and other retinoic acid sensitive protein (CD-RAP, 44% identity and 64% similarity over 126 amino acids) and other retinoic acid sensitive or melanoma in the prophylaxis, treatment (including gene therapy) and diagnosis of disorders and diseases caused by, or involving, cartilage development and maintenance, inhibition of melanoma cell growth and tumours, inncluding neuroectodermal tumours such as gliomas. The polynucleotides can also be used to design probes
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                                                                                        Claim 1; Page 115; 119pp; English.
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DNAS. The MLP proteins and DNAS have antiinflammatory and cardiant activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAS can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic angiogenesis.

AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
                                                                                                                                                                                                                                                                                                                                                                                                            Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and joint
                                                                                                                                                                                                                                                                                         Yoshimura K;
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                                                                                                                                                                                                                                                                                           Mogi
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                                              WO200102564-A1.
Homo sapiens
                                                                                                                                                                                          30-JUN-1999;
                                                                                            11-JAN-2001.
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WPI; 2001-483233/52.
                P-PSDB; AAB82671.
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Growth regulatory-like polypeptide; human; cartilage; melanoma; neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;
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Human growth regulatory-like polypeptide cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Arterburn MC,
                                                                                                                                   Location/Qualifiers 33..419
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02-MAY-2000; 2000US-0563786
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33..101
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102..416
/*tag= c
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                                                                                                  Homo sapiens
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e.g. Alzheimer's disease, cancer, autoimmune disorders, hyperproliferative disorders, coagulation disorders, and nervous system Isolated human growth regulatory-like polypeptide useful for treating disorders

Liu C;

Claim 1; Page 115-116; 119pp; English.

human growth regulatory like polypeptide (GRLP, see AABB2671).
The sequence was assembled using human thymus CDNA library-derived
Hyseq clone identification number 1637272 (see AAB2631) as seed,
using software programs to pull additional sequences from Hyseq's
proprietary database containing expressed sequence tag sequences,
and by gel sequencing using primers to extend both 5' and 3' ends.
The predicted protein has a mol.wt. of 14 kDa unglycosylated. GRLP
belongs to the same protein family as growth regulatory proteins
c growth factors, human melanoma derived growth regulatory protein
precursor (64% similarity and 45% identity over 111 amino acids)
or melanoma inhibitory activity, cattle cartilage-derived
c retinoic acid sensitive protein (CD-RAP, 44% identity and 64%
similarity over 126 amino acids) and other retinoic acid-sensitive
proteins. GRLP polypeptides and polynucleotides of the invention growth and tumours, including neuroectodermal tumours such as glidmas. The polynucleotides can also be used to design probes and primers, for chromosome and gene mapping, in the recombinant production of protein, in the generation of antisense, ribozyme and production of protein, in the generation of antisense, ribozyme and peptide-nucleic acid molecules, and to produce transgenic animals. They may also have cytokine and cell proliferation or ribozyme and differentiation activity, stem cell growth factor activity, haematopoiesis regulating activity, tissue growth activity, immunosuppressive or immunostimilate activity, nemostatic and thrombolytic activity, use in cancer diagnosis and therapy, activity, and treatment of leukaemia, nervous system disorders, arthritis and inflammation. GRLP can be used in the prophlaxis, treatment (including gene therapy) and diagnosis of disorders and diseases caused by, or involving, cartilage development and maintenance, inhibition of melanoma cell The present sequence is that of a novel nucleic acid encoding

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
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                                         Length 1201;
                                                              Indels
        Sequence 1201 BP; 357 A; 188 C; 275 G; 381 T; 0 other;
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                                        Score 330; DB 22
Pred. No. 5.1e-97
                                               100.0%; Pred. m.
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Tanaka H;
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The present invention describes novel MLP proteins and their encoding DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic angiogenesis. AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
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                                                                                                                                                                                                                aacgttaaaaaagggcagcagatctatgtgtactcaaagctggtaaaagaaaatggagct
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                                                                                                                                                                                        0;
                                                                                                                                                            Length 330;
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                                                                                                                                                            DB 22;
                                                                                                                                                                                       48;
                                                                                                                       Sequence 330 BP; 91 A; 60 C; 92 G; 87 T; 0 other;
                                                                                            in the exemplification of the present invention.
                                                                                                                                                           76.4%; Score 252.2; DB ilarity 85.4%; Pred. No. 5.7e-72; Conservative 0; Mismatches 48
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P-PSDB; AAB69125.
                                                                                                                                                            Query Match |
Best Local Similarity
Matches 281; Conserv
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cardiant; gene t
inhibitor; ds.
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                                                                                                                 The present invention describes novel MLP proteins and their encoding bulss. The MLP proteins and DNAs have antiinflammatory and cardiant activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic angiogenesis. AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
                                           joint
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       Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and
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                                                                                                                                                                                                                            in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                    76.4%; Score 252.2; DB 2:
85.4%; Pred. No. 6.1e-72;
Live 0; Mismatches 48
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Matches 281; Conservative
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AAF$9063 to AAF$9099 and AAB$9122 to AAB$9132 represent sequences used
                                                                                                              Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and joint
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                                            Yoshimura
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                                           Noguchi Y,
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                                                                                                                                                                                                                                                                                                                                                                                      76.4%; Score 252.2; DB 22;
85.4%; Pred. No. 9.2e-72;
live 0; Mismatches 48; 1
                                                                                                                                                                                                                                                                                                                  the exemplification of the present invention.
                                           Mogi S,
                                                                                                                                                                                   Example 2; Page 100-101; 111pp; Japanese.
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                                        Nishi K,
              (TAKE ) TAKEDA
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The present invention describes novel MLP proteins and their encoding DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic anglogenesis. AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
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                                                                                                                                                    Yoshimura K;
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                                                                                                                                                   Noguch1 Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              the exemplification of the present invention.
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0; Mismatches
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                                                                                                                                                   Ogi K, Ohkubo S,
                                                                                                                                                                                                                                                                                                                        Claim 12; Page 107; 111pp; Japanese.
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                                                         29-JUN-2000; 2000WO-JP04278.
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                                                                                                                      (TAKE ) TAKEDA CHEM IND LTD
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es 279; Conserv
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The present invention describes novel MLP proteins and their encoding DNAS. The MLP proteins and DNAS have antiinflammatory and cardiant excitvities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAS can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic angiogenesis.
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            IIA; melanoma inhibitory activity; cancer; bone disease;
disease; pathologic angiogenesis; diagnosis; antiinflammatory;
int; gene therapy; secretory cell function regulator; promoter;
                                                                                                                                                                                                                                                                  Noguchi Y,
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                                                                                                                                                                                                                                                                                                                                                      low-toxicity
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                                                                                                                                                                            29-JUN-2000;
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                                           cardiant;
inhibitor;
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                                                                                      Rattus sp.
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Score 249; DB 22;
Pred. No. 6.7e-71;
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ilarity 84.8%;
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The present invention describes novel MLP proteins and their encoding DNAs. The MLP proteins and DNAs have antiniflammatory and cardiant activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic angiogenesis.

AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
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Pred. No. 9.3e-
0; Mismatches
                                                                                      Rat MLP nucleotide sequence SEQ ID NO:41.
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AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
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Pred. No. 5e-53;
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83.98;
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Sequence:

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melanoma-derived growth regulatory protein MIA - human C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 04-Mar-2000 C.Accession: 138019; 840238 R.Blesch, A.; Bosserhoff, A.K.; Apfel, R.; Behl, C.; Hessdoerfer, B.; Schmitt, A.; Ja Cancer Res. 54, 5695-5701, 1994 A.; Tiller: Cloning of a novel malignant melanoma-derived growth-regulatory protein, MIA A. Reference number: 138019; MUID:95007612
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N.Alternate names: finger protein vav
C.Specias: Homo sapiens (man)
C.Specias: Homo sapiens (man)
C.Sacession: B39576; S05382
R.Katzav, S.; Cleveland, J.L.; Heslop, H.E.; Pulido, D.
Mol. Cell. Biol. 11, 1912-1920, 1991
A.Title: Loss of the amino-terminal helix-loop-helix domain of the vav proto-oncogene
A.Reference number: A39576; MUID:91172176
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A; Residues: 1-61 < KAT>
A; Coss.references: GB:M59834; NID:g340189; PIDN:AAA63267.1; PID:g340190
A; Orces the authors translated the codon CAA for residue 6 as Glu, CAG for residue 13
A; Note: the authors translated the codon CAA for residue 6 as Glu, CAG for residue 13
R; Katzav, S.; Martin Zanca, D.; Barbacid, M.
EMBO J. 8, 2283-2290, 1989
A;Title: vav, a novel human oncogene derived from a locus ubiquitously expressed in h
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probable
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A;Molecule type: mRNA
A;Residues: 1-131 <RES>
             C75325
T33655
S24156
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                                                                                                          Search time 16.58 Seconds
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              GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                                                        September 23, 2002, 09:36:50
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                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Oncogene 7, 611-618, 1992

A.Title: The hematopoletically expressed vav proto-oncogene shares homology with the A.Fitle: The hematopoletically expressed vav proto-oncogene shares homology with the A.Fitle: The hematopoletically E.B. 1015-92288488

A.Contents: annotation: the authors note the frameshift difference with sequence in A A.Note: the complete sequence was submitted to Genbank; see $36941

C.Genetics:
A.Gene: vav
C.Superfamily: vav transforming protein; CDC24 homology; protein kinase C zinc-bindin C.Keywords: phosphoprotein; transforming protein; zinc finger
F.132-176/Region: leucine-rich
F.132-176/Region: acidic
F.134-458/Domain: CDC24 homology <CD24>
F.136-540/Region: proline-rich
F.536-540/Region: nuclear location signal
F.515-566/Region: zinc finger CCCC motif F.515-566/Region: zinc finger CCCC motif F.515-566/Region: zinc finger CCCC motif F.515-566/Region: proline-rich
F.553-566/Region: proline-rich
F.553-566/Region: proline-rich
F.553-660/Region: proline-rich
F.553-660/Region: proline-rich
F.553-66/Region: proline-rich
F.553
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A.Title: Identification of VAV2 on 9q34 and its exclusion as the tuberous sclerosis A; Reference number: I51940; MUID:95283235
A; Accession: I51940
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C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 16-Jul-1999
C;Accession: I51940
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A.Molecule type: mRNA
A.Molecule type: mRNA
A.Cross-references: GB:S76992; NID:g913345; PIDN:AAB34377.1; PID:g913346
C.Genetics:
A.Gene: GDB:VAV2
A.Gene: GDB:VAV2
A.Gene: GDB:VAV2
A.Gene: GDB:VAV2
A.Gene: GDB:VAV4
C.Superfamily: vav transforming protein; CDC24 homology; protein kinase C.Superfamily: vav transforming protein; CDC24
C.Superfamily: V
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26.3%; Pred. No. 2.3;
:ive 21; Mismatches
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                                                                                                                A; Molecule type: mRNA
A; Residues: 62-839 <KAT2>
A; Cross-references: EMBL:X16316
B; Adams, J. M.; Houston, H.; Allen, J.; Lints, T.; Harvey, R.
Oncogene 7, 611-618, 1992
A; Title: The hematopoletically expressed vav proto-oncogene shares homology with the dbl
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*Residéos: 1-323, 'DILMVPMORVLKYHLLLQELVK', 346-347, 'QDAT', 352,'K', 354,'N', 355-453,'R', 45
A;Cross-references: EMBL:X64361; NID:955220; PIDN:CAA45713.1; PID:955221
R;Adams, J.M.; Houston, H.; Allen, J.; Lints, T.; Harvey, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Superfamily: var transforming protein; CDC24 homology; protein kinase C zinc-binding C; Superfamily: var transforming protein; zinc finger C; Keywords: phosphoprotein; transforming protein; zinc finger C; Keywords: phosphoprotein; transforming protein; zinc finger CDC24 homology cDC24 homology cDC24 homology cCD24 homology cCD24 homology cCC2 motif concern in protein kinase C zinc-binding repeat homology cK22> 522-542/Region: zinc finger CCCC motif concern concer
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A; Molecule type: mRNA
A; Residues: 1-844 (COP)
R; Katzav, S.; Oleveland, J.L.; Heslop, H.E.; Pulido, D.
Mol. Cell. Biol. 11, 1912-1920, 1991
A; Frêference number: A39576; MUID:91172176
A; Reference number: A39576; MUID:91172176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Note: in the sequence from mouse the authors find three additional nucleotides that occurred in the published human sequences
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C;Species: Mus musculus (house mouse)
C;Dacte: 03-May-1994 #sequence_revision 16-Feb-1996 #text_change 18-Jun-1999
C;Accession: A61187; A39576; S36541; S23669
COppola, J; Bryant, S; Koda, T; Conway, D; Barbacid, M.
A;Title: Mechanism of activation of the vav protooncogene.
A;Reference number: A61187; MUID:91299578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-28, 'E',30-93 <KAT>
A;Cross-references: GB:M59833; NID:g202343; PIDN:AAA63402.1; PID:g202344
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Best Local Similarity 32.9%; Pred. No. 0.68;
Matches 23; Conservative 13; Mismatches 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GDB:127112; OMIM:164875
A;Map postition: 19p13.3-19p13.3
C;Superfamily: vav transforming protein; CDC
C;Keywords: phosphoprotein; transforming proc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: S23669; MUID: 92228488
A; Contents: annotation
                 A; Reference number: S05382; MUID: 90005432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: S36941
A; Accession: S36941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: GDB: VAV1; VAV
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A;Introns: 1/3; 41/3; 72/2; 103/2; 162/3; 184/1; 217/1; 296/1; 340/3; 390/3; 447/3; 5 C;Superfamily: protozoan myosin heavy chain IB; myosin motor domain homology; SH3 hom F;14-674/Domain: myosin motor domain homology <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: T48525
K; Bevan, M.; Hibert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancro
submitted to the Protein Sequence Database, April 2000
A; Reference number: 224490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     asparagine synthase (glutamine-hydrolyzing) (EC 6.3.5.4) MJ1116 [similarity] - Methan C; Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 09-Jun-2000 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: C64439
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc
                            RiLee, W.L.; Ostap, E.M.; Zot, H.G.; Pollard, T.D. submitted to the EMBL Data Library, August 1998
A; Description: Hydrodynamic and ligand binding properties of Acanthamoeba myosin-IA (A; Reference number: Z21216
A; Reference number: Z21216
                                                                                                                                                                                                                                                               A:Residues: 1-1215 <LEE>
A:Residues: 1-1215 <LEE>
A:Cross-references: EMBL:AF085185; NID:g3599477; PID:g3599478; PIDN:AAC35357.1
A:Experimental source: strain Neff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | | | | | | | | | : :::| | | | | | :1158 PPTVGRCRALYDYGAQEADELTLREGDVIDVIQK------SGEWWEGTLNGK------T 1204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein T22P22.50 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
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A;Experimental source: cultivar Columbia; BAC clone T22P22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.6%; Score 74.5; D 28.6%; Pred. No. 18; Live 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Mismatches
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Pred. No. 4
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Note: T22P22.50
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37.2%;
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Best Local Similarity 28.6%
Matches 20; Conservative
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Best Local Similarity 37.27
Best Local 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 GYFPRNLVKE 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: T48525
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                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: MIA
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C64439
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A; Molecule type: DNA
A; Residues: 1-1589 <-PAU>
A; Molecule type: DNA
A; Residues: 1-1589 <-PAU>
A; Coss-references: EMBL:U17247; NID:9577216; PIDN:AAB67360.1; PID:9577222; GSPDB:GN0001
A; Cross-references: EMBL:U17247; NID:9577216; PIDN:AAB67360.1; PID:9577222; GSPDB:GN0001
B; Camonis, J.H.; Kalekine, M.; Gondre, B.; Garreau, H.; Boy-Marcotte, E.; Jacquet, M.
EMBO J. 5, 375-380, 1986
A; Title: Characterization, cloning and sequence analysis of the CDC25 gene which control
A; Reference number: A23444
A; Molecule type: DNA
A; Residues: 1-496, YY, 498-953, LSVIMNLSR', 964-1589 <-CAM>
A; Residues: 1-496, YY, 498-953, LSVIMNLSR', 964-1589 <-CAM>
A; Residues: 1-496, YY, 498-953, LSVIMNLSR', 964-1589 <-CAM>
A; Cross-references: EMBL:X03579; NID:93483; PIDN:CAA27259.1; PID:93484
B; Danial, J.H.
Curr. Genet. 10, 879-885, 1986
A; Title: The CDC25 Start" gene of Saccharomyces cerevisiae: sequencing of the active C-A; Reference number: S43051; MUID:88194639
A; Molecule type: DNA
A; Residues: 877-1589 <-CAN>
A; Cross-references: EMBL:X03579
                                                                                                                          RESULT 5

ROBYCS

Cell division control protein CDC25 - yeast (Saccharomyces cerevisiae)

N.Alternate names: protein L2142.6; protein YLR310c

C; Species: Saccharomyces cerevisiae

C; Species: Saccharomyces cerevisiae

C; Species: Saccharomyces cerevision 31-Mar-1993 #text_change 21-Jul-2000

C; Accession: A26596; S51442; A23444; A33091; S47990

R; Broek, D.; Toda, T.; Michaeli, T.; Levin, L.; Birchmeier, C.; Zoller, M.; Powers, S.;

A; Title: The S; cerevisiae CDC25 gene product regulates the RAS/adenylate cyclase pathwa

A; Reference number: A26596; MUID: 87131091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unction:
| positive control of level of cellular cAMP at the stage at which the cell serification:
| positive control of Level of cellular cAMP at the stage at which the cell solperfamily: | budding yeast CDC25; CDC25-type guanine nucleotide exchange activator hom C; Keywords: cell cycle control; transmembrane protein
| F; 65-123/Domain: SH3 homology <SH3>
| F; 65-123/Domain: CDC25-type guanine nucleotide exchange activator homology <SOS>
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C;Species: Acanthamoeba castellanii
C;Date: 29-Oct;1999 #sequence_revision 29-Oct-1999 #text_change 08-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule typė: DNA
A; Residues: 1-1589 <BRO>
A, Cross-references: EMBL:M15458; NID:9171184; PIDN:AAA34478.1; PID:9171185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amitted to the EMBL Data Library, November 1994
A;Description: |The sequence of S. cerevisiae cosmid L2142.
A;Reference number: S51437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative 21; Mismatches
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;Cross-references: SGD:S0004301; MIPS:YLR310c
;Map position 12R
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| :|:|| |:|:
862 GRIGWFPSTYVEEEGI 877
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nes 23; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            auley, A.
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Balbian ring 1 chain - midge (Chironomus tentans) (fragment)
C;Species: Chironomus tentans
C;Date: 23-aug-1987 #sequence_revision 23-aug-1987 #text_change 21-Jul-2000
C;Accession: A23516
R;Hoog, C.; Engberg, C.; Wieslander, L.
Nucleic Acids Res. 14, 703-719, 1986
A;Title: A BR 1 gene in Chironomus tentans has a composite structure: a large repetit A;Reference number: A23516; MUID:86120366
A;Accession: A23516
A;Molecule type: DNA
A;Residues: 1-383 <HOO>
                                                                                        84 LRNGSGRVKEKIRDIFSGVIYDREIDELAALVYYPEDKLKLIKHDFDAKEALNE 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A)Cross-references: GB:x03490;
A)Note: the authors translated
C)Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Introns: 273/1
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C; Species: C; Species: Bacillus subtilis
C; Species: C; Species: Species: C; Species: Species: C; Species: C; Species: Species: Species: Species: C; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-67] - KUN.>
A; Cross-references: GB: Z99124; GB: AL009126; NID: 92636442; PIDN: CAB16056.1; PID: 92636566
A; Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Description: catalyzes the hydrolysis of fructose-1, 6-bisphosphate to fructose-6-phosp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Note: requires manganese ion for stability and phosphoenolpyruvate for activation C;Superfamily: Bacillus subtilis fructose-bisphosphatase; phosphoesterase core homology C;Keywords: carbohydrate metabolism; gluconeogenesis; metalloprotein; phosphoric monoest
                                                                                                        A; Molecule type: DNA
A; Residues: 'MRD',1-541 < BUL>
A; Residues: 'MRD',1-541 < BUL>
A; Residues: 'MRD',1-541 < CB:L77117; NID:92826365; PIDN:AAB99117.1; PID:91591755; A; Mote: an incorrect initiation codon was used C; Genetics:
A; Map position: REVIOS81315-105681
C; Superfamily: asparagine synthase (glutamine-hydrolyzing)
C; Keywords: asparagine biosynthesis; ligase
F:2-541/Product: asparagine synthase (glutamine-hydrolyzing) #status predicted <MAT>
F:2/Active site: Cys #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 IFMDRLAS------KKLCADDEC-VYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKL 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fructose-bisphosphatase (EC 3.1.3.11) [validated] - Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29;
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                                                                                A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.1%; Score 71.5; D 22.8%; Pred. No. 19; Live 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 71.5; 1
Pred. No. 15;
A; Reference number: A64300; MUID:96337999
A; Accession: C64439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.1%;
25.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27; Conservative
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26; Conservative
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Best Local Similarity
Matches 27; Conservat
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A,Gene: fbp; yydE
C,Function:
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Matches
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NID:97043; PIDN:CAA27206.1; PID:9769785 the codon GAA for residue 118 as Gly and TTC for resid

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ATP-dependent RNA helicase, superfamily II [imported] - clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001 C; Accession: G96995 R; Nolling, J; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; L.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J; Bennett, G.N.; Koonin, E.V.; Smith, D.R. J; Benteriol. 183, 4813-4839, 2001 A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium A; Reference number: A96900; MuID:21359325; PMID:21359325 A; Accession: G96995 A; A; A; A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-585 < KUR>
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A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC0778
                                                                                                                                                                                                                                                                                                                                                       303 DKDCCKKNCNCDGAKF------PECEESNSKQSGMFDILAKLFKPQG-GDFEA 348
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                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                     6 DRLASKKLCADDECVYTISLAŞAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWA 65
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                                                                                                                   Query Match 12.0%; Score 71; DB 2; Length 383; Best Local Similarity 28.0%; Pred. No. 12; Matches 26; Conservative 10; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.0%; Score 71; DB 2; Length 585; 29.4%; Pred. No. 19; ive 13; Mismatches 37; Indels
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C; Superfamily: unassigned Balbiani ring proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        349 GSVEVDGKK-----LSPEKKEKFGKALQDAVK 375
                                                                                                                                                                                                                                                                                                                                                                                                                                          66 GSVYGDGQDEMGVVGYFPRNLVKEQRVYQEATK 98
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Matches 30; Conservative
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35 YLQLLAQKYDCEEKVVTEIINLKA------ILNLPKGTEHFVSDLHGEYQAFQHV 83

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4 FMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYS---

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C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Accession: D86758
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                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 26.98
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Matches 28; Conserv
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C; Keywords: nucleomorph
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                                                              C;Species: Sulfolobus Solfataricus
C;Species: Sulfolobus Solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001
C;Accession: C90186
R;She, O.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chandon, I.; Jeffriss, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, Farett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
Submitted to GenBank, April 2001
A;Pescription: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: C90186
A;Accession: C90186
A;Status: preliminary
A;Accession: C90186
A;Residues: 1-769
A;Residues: 1-769
A;Residues: 1-769
A;Residues: 1-769
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A; Cross-references: GB:AE001779; GB:AE000512; NID:g4981777; PIDN:AAD36302.1; PID:g498178
A; Experimental source: strain MSB8
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                          Gene: SSO0421 |
uperfamily: transitional endoplasmic reticulum ATPase; FtsH/SEC18/CDC48-type ATP-bind
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C,Accession: D72278
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome **Reference number: A72200; MUID:99287316
Ccession: D72278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                endo-1,4-beta-mannosidase - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun_1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 12.0%; Score 71; DB 2; Length 769; Best Local Similarity 35.0%; Pred. No. 25; Matches 28; Conservative 10; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49 YVYSKLVKENG-----AGEFWAGSVYGDG--QDEMGVVGYFPRNL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37;
                                          AAA family ATPase [imported] - Sulfolobus solfataricus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 AQV-QDATKVVLAPTQPISF 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 QRVYQEATKEV--PTTDIDF 107
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Best Local Similarity
Matches 32; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Genetics:
A;Gene: TM1227
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R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Eh Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: D86758
A;Accession: D86778
A;Accession: D86778
A;Accession: Call A;Accession: A;Acce
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A;Title: The highly reduced genome of an enslaved algal nucleus.
A;Reference number: A99082; MUID:11323671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE005176; PID:g12724022; PIDN:AAK05166.1; GSPDB:GN00146
A;Experimental source: strain IL1403
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A Modecule type: DNA
A Residues: 1-295 < LOUD>
A Cross-references: GB:AJ010592; NID:g12580757; PIDN:CAC27075.1; GSPDB:GN00151
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C;Superfamily: kinase-related transforming protein; protein kinase homology
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A;Note: a nucleomorph is dillardia theta
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 15-Jun-2001
C;Accession: F90113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 LASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGA--GEFWA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 LASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYFPR 84
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C;Keywords: glycosyltransferase; pentosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.9%; Score 70; DB 2; 26.9%; Pred. No. 7.7; iive 15; Mismatches 4
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72 12.2 407 17 09HJF2 72 12.2 615 10 094E30 72 12.2 638 10 09ATQ5 71.5 12.1 671 16 045597	71.5 12.1 839 10 Q94F88 71 12.0 383 5 Q23770 C	71 12.0 585 16 097KYB 71 12.0 585 10 09FU01 71 12.0 769 17 097Z29 71 12.0 2087 11 09WUE8	111111	70.5 11.9 209 16 09CGM8 70 11.9 209 16 09COM8	70 11.9 709 11 Q94047 70 11.9 905 11 Q94V47 70 11.9 11 G94V47	70 11.9 1217 11 09WVE9 70 11.9 1240 11 094VL4	70 11.9 1806 11 Q9WUY7 69.5 11.8 295 10 Q9AVZ6 60.5 11.8 66.6 0204VZ6	11.8 1199 11.7 328 11.7 338	ALIGNMENTS	RESULT 1	,	AC Q9J109; DT 01-0CT-2000 (TIEMBIrel 15, Created) DT 01-0CT-2000 (TIEMBIrel 15, Last segmence undate)	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; OC Mesocricetus. OX NCBI TaxID=10036;				DR Pfam; PF00018; SH3; 1. DR SMART; SM00326; SH3; 1. DB DPGTTE: 0550007: 5H3: 1.	NON_TER 1 1 1 NON_TER 96 96	SQ SEQUENCE 90 AA; 10/50 MW; E/B450C3B55U5BFB CRC04; Query Match 38.4%; Score 226.5; DB 11; Length 96; Rest Local Similarity 46.4%; Pred, No. 8 9e-18.	45; Conservative 1	OY 8 LASKKLCADDECVTISLASAQEDYNAPDCRFINVKGQQIYVYSKLVKENGAGE-FWAG 66	1 DADKALDEGENETERANAMEDINAFDEKETITIRKENYYYYYYYY NGARANGANAMENGAN
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	OM protein - protein search, using sw model	Run on: September 23, 2002, 09:37:20 ; Search time 24.59 Seconds (without alignments) 773:869 Million cell updates/sec	Title: Perfect score: 590 Sequence: 1 HGIFMDRLASKKLCADDECVRVYQEATKEVPTTDIDFFCE 110	Scoring table: BLOSUM62 Gapext 0.5	eqrched: 562222 seqs, 172994929 residues	al number of hits satisfying chosen parameters: 562222	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 00% Maximum Match 100% Listing first 45 summaries	Database : . SPTREMBL_19:* 1:					Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES	Result Query No. Score Match Length DB ID Description	226.5 38.4 96 11 09J109 185.5 31.4 119.4 096PFF	181 30.7 137 11 0921X3 0951X3 0951X3 11 0951X3 11 0951X3 11 0951X3 11 0951X40	100.21 20.01 20.00	77 13.1 331 2 <u>0</u> 93JT7 74.5 12.6 1215 5 077202	74 12.5 308 10 Q9LXG4 Q91yg4 74 12.5 2161 4 Q9Y566 Q9Y565 73 12.4 636 11 OGFW78 OGF+56	73 12.4 643 10 Q9FU04 Q9FU04 C172a C

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23 ISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAG-EFWAGSVYGD--GQDEMGVV 79
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
MELANOMA INHIBITORY ACTIVITY PROTEIN (FRAGMENT).
Tetraodon nigroviridis (Green puffer). Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.6%; Score 168.5; DB 13; Length 43.3%; Pred. No. 2.4e-11; Live 15; Mismatches 29; Indels
                                                                                                                                                                                                                                                              SECUENCE FROM N.A.
TISSUE-EMBRYO;
BOSSCHOff A.K., Buettner R.;
"Characterization of the MIA gene family.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF390177; AAL26992.1; -
EMBL; AF390177; AAL26992.1; -
SEQUENCE 119 AA; 13397 WW; 589F390C0B49D1C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Busserhoff A.K., Buettner R.;
Characterization of the MIA gene family.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF390176; AAL26691.1; -.
SEMBL, SEQUENCE 88 AA: 10080 MW; C355C1FE04DA22EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MELANOMA INHIBITORY ACTIVITY PROTEIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 VYGDGQDEMGVVGYFPRNLVKEQRVYQEATKEVPTTDIDFFC 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                29.1%; Score 171.5; DB 11; 39.2%; Pred. No. 1.6e-11; iive 14; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88 AA.
                                           119 AA
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Best Local Similarity 43.3'
Matches 39; Conservative
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                                           PRELIMINARY;
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                                                                                                                                                                                                                         NCBI_TaxID=10090;
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                                         0912V0
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Matches
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  RESULT
Q912V0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 MPKLADWKLCADEECSHPISMAVALQDYVAPDCRFLTIYRGQVVYVFSKL---KGRGRLF 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
MCBI_TaxID-10090;
                                                                                                                                                                                                                                                                Euteleostomi;
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                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelé
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.4%; Score 185.5; DB 4; Length 40.2%; Pred. No. 4.5e-13; Live 15; Mismatches 37; Indels
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                                                                                                                                                                                                                                                                                                                                                                             Bosserhoff A.K., Buettner R.; "Characterization of the MIA gene family."; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AF190175; AAL26990.1; "SEQUENCE 119 AA: 13535 MW; AEF529762D880AC5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
Submitted (JUL-2001): ARH09815.1; -.
EMBL; BC009815; ARH09815.1; -.
SEQUENCE 137 AA; 15441 MW; 971415552E6FD536 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILAR TO CARTILAGE DERIVED RETINDIC ACID SENSITIVE
                                                                                                                                                          01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | | | | : : | | | | : : | | | 58 SVQGDYXGDLAARLGYFPSSIVREDQILKPGKVDVKT 94
                                                                                                                         AA
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                                                                                                                    119
                                                                                                                                                                                                                     MELANOMA INHIBITORY ACTIVITY PROTEIN 2.
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Best Local Similarity 55.44
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41; Conservative
                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                   TISSUE-EMBRYO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WAGSV 68
                                                                                                                                         Q96PC5;
                                                                                                                    Q96PC5
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RESULT Q921X3

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3;

Gaps 67

6

DB 11; Length 119;

4;

Gaps

7;

Length

m

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A51B757DA543BA6C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-DDY; TISSUE-TESTIS;
MEDLINE-97190224; PubMed-9038379;
        83727 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19434 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:98923; Vav.
InterPro; IPR000980; SH2.
InterPro; IPR001452; SH3.
Pfam; PF00017; SH2; 1.
PRINTS; PF00452; SH3DOMAIN.
SMART; SM00252; SH3DOMAIN.
SMART; SM00252; SH2; 1.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50001; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 16, C
(TrEMBLrel. 16, I
(TrEMBLrel. 19, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oncogene 14:713-720(1997).
EMBL; D83266; BAA18950.1; -HSSP; Q60631; 1GBQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 31.49
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                          710 YVEED--YSE 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 YVEED--YSE 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166 AA;
        719 AA;
                                                                                                                                                                                                                                                                                       86 LVKEORVYQE 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 LVKEQRVYQE 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9H803;
01-MAR-2001
01-MAR-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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Q9H803
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 VYTIŠLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVV 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                           Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S., Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H., Lauber J., Dusetzerhoeft A., Beyer A., Koehrer K., Strack N., Mewes H.W., Ottemwaelder B., Obermaler B., Tampe J., Heubner D., Wambutt R., Korn B., Klein M., Poustka A.;

"Towards a Catalog of Human Genes and Proteins: Sequencing and Analysis of 500 Novel Complete Protein Coding Human cDNAS.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50002; SH3; 1.
PROSITE; PS50002; SH3; 1.
PROSITE; PS50084; WD_REPEATS_REGION; 1.
HYDOCTHETICAL Profesh; Repeat; WD repeat.
SEQUENCE | 1196 AA; 137114 MW; E27E3FB1D7932024 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013361; AAH13361.1; -.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Res 11:422-435(2001).
-!- SIMILARITY: CONTAINS 4 WD REPEATS (TRP-ASP DOMAINS)
                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 137.1 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETIÇAL 83.7 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.0%; Score 88.5; DB 33.3%; Pred. No. 0.57; iive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          719 AA
                                PRT; 1196 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
TISSUE-PLACENTA, AND CHORIOCARCINOMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-21154917; PubMed-11230166;
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1099 GYFPANHVASETLYQELPPEI 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 GYFPRNLVKEORVYOEATKEV 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; FUGAGI, 1531.
InterPro; IPR001452; SH3.
InterPro; IPR001680; WD40.
Pfam; PF00018; SH3; 1.
Pfam; PF00400; WD40; 4.
PRINTS; PR00452; SH3DOMAIN.
SMART; SM00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AL136797; CAB66731.1;
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                             PRELIMINARY;
                                                                                                                                                                                                         Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 27; Conserv
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P06241; 1SHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-9606;
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SEQUENCE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.
                             99н0н2
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Q96D37
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661 AKARYDFCARDRSELSLKEGDII----KILNKKGQQGWWRGEIYGR------VGWFPAN 709
                                                                        Gaps
                                                                                                                                             26 ASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYFPRN 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 ASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYFPRN 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathl; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Okumura K., Kaneko Y., Nonggushi K., Nishiyama H., Yokoi H., Higuchi T., Itoh K., Yoshida O., Miki T., Fujita J.; "Expression of a novel isoform of Vav, Vav-T, containing a single Srchomology 3 domain in murine testicular germ cells.";
Query Match 14.7%; Score 86.5; DB 4; Length 719; Best Local Similarity 32.9%; Pred. No. 0.5; Matches 23; Conservative 13; Mismatches · 21; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
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Last annotation update)
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DB 2; Length 331;

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13.1%; Score 77; DB 325.6%; Pred. No. 2.2; ive 22; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS: PRO0193; MYOSINHEAVY.
PRINTS: PRO0452; SH3DOMAIN.
ProDom; PD000355; myosin_head;
    Query Match
Best Local Similarity 25.69
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00242; MYSC; 1.
SMART; SM00326; SH3; 1.
PROSITE; PS50002; SH3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-NEFF;
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Q9LYG4
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A Isogael T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
A Mishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
A Magatsuma M., Hosolii T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
A Takahashi M., Chibba Y., Ishida S., Murakawa Y., Chiba Y., Tishida S., Murakawa Y., Saito K.,
A Mamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
A Mamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
A Minomiya K., Iwayanagi T.;
A Willomiya K., Iwayanagi M., Andoli S.,
A Willomiya K., Iwayanagi T.;
A Willomiya K., Iwayanagi T.;
A Willomiya K., Iwayanagi T.;
A Willomiya K., Iwayanagi K., Iwaya K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 VYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVV 79
                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas stutzeri (Pseudomonas perfectomarina).
Bacteria: Proteobacteria: gamma subdivision: Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 14.0%; Score 82.5; DB 4; Length 498; Local Similarity 32.1%; Pred. No. 0.89; les 26; Conservative 12; Mismatches 32; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lin M., Gao L., Desnoues N., Elmerich C.;
"Dicarboxylic acid transport in Pseudomonas stutzerl.";
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ313422: CAC44171.1; -.
SEQUENCE 331 AA; 36729 MW; CB893C98508BEC39 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  498 AA; 57011 MW; 0D2F58A28A4553AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PROBABLE C4 DICARBOXYLATE BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               331 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 GYFPRNLVKEQRVYQEATKEV 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPOTHETICAL 57.0 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                          TISSUE-EMBRYO;
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Matches

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Lee W.-L., Ostap E.M., Zot H.G., Pollard T.D.;
"Hydrodynamic and ligand binding properties of Acanthamoeba Myosin-IA GPA/SH3 domain.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF085185; AAA35357.1; ...
HSSP; P08799; 1MND.
InterPro: IPR001609; myosin_head.
InterPro: IPR001422; SH3.
Pfam; PF00063; myosin_head; 1.
Pfam; PF00063; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1158 VPTVGRCRALYDYGAQEADELTLREGDVIDVIQK-----SGEWWEGTLNGK-----T 1204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        r22P22_50.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
22; Gaps
                                                    5 MDRLASKKLCADDECVYTISLASAQEDYNAPDCRFI-----NVKKGQQIYVYSKLVKENG 59
                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 VYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVV 79
                                                                                                                                                          60 AGE----FWAGSVYGDGQDE----MGVVGYFPRNLVKEQRVYQEATKEVPTTDIDF 107
                                                                                                                                                                                           Query Match 12.6%; Score 74.5; DB 5; Length 1215; Best Local Similarity 28.6%; Pred. No. 21; Matches 20; Conservative 12; Mismatches 25; Indels 13
     43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1215 AA; 134103 MW; FEFBFCC2EF936C72 CRC64;
                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL 34.0 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                             PRT; 1215 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acanthamoeba castellanii (Amoeba).
Eukaryota; Acanthamoebidae; Acanthamoeba.
NCBI_TaxID=5755;
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093JT7; Q93JT7 SULT 10

593JT7

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AC 099
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                                                                          SEQUENCE FROM N.A.

Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
Bancroft I., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

Zitzer H., Hoenck H.-H., Richter D., Kreienkamp H.-J.;

"The somatostatin receptor interacting protein (SSTRIP) defines a novel family of multidomain postsynaptic density proteins.";

Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF163302; AAD45121.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 2161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SOMATOSTAȚIN RECEPTOR INTERACTING PROTEIN SPLICE VARIANT A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5FEFC969CBE98701 CRC64;
                                                                                                                                                                                                                                                                                                              44 KGQQİYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYFPRNL 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 74; DB 10;
Pred. No. 4.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 2161 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          091566;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
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PROSITE; PS50297; ANK_REP_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Receptor; Repeat.
2161 AA; 225019 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.5%;
37.2%;
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IPR001660; SAM.
IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS50106; PDZ; 1
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PROSITE; PS50106; PDZ;
PROSITE; PS50002; SH3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00248; ANK; 3
SMART; SM00228; PDZ; 1
SMART; SM00454; SAM; 1
SMART; SM00326; SH3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00023; ank; 6.
Pfam; PF00595; PDZ; 1.
Pfam; PF00536; SAM; 1.
Pfam; PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P06241; 1SHF
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-9606;
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Best Local Simi
Matches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANK repeat;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09X566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168
    DDT TO DD
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Gaps
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                                                                                                                                                                                      pUTATIVE RECEPTOR KINASE.
P0698603.32 OR P0494A10.10.
Oryza sativa (Rice).
Spermatophyta; Vildiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRALM-CV. NIPPONBARE;
SABAKI T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRALM-CV. NIPPODNBARE;
SASAKI T., Matsumoto T., Yamamoto K.;
Noryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone:P0494A10.";
Submitted (JUN 2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP0022747; BAB17348.1;
EMBL; AP001241; BAB55470.1;
HSSP; P08631; 1AD5.
                                                                                                                                                                                                                                                                                                                                                                                                   clone:P0698G03.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
ATP-binding; Kinase; Receptor; Transferase.
ATP-binding; Kinase; Receptor; Transferase.
SEQUENCE 636 AA; 70968 WW; E6805D9EIDP43462 CRC64;
                                                                                                                                                Created)
Last sequence update)
Last annotation update)
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InterPro: IPR002290; Ser_thr_pkinase.
InterPro: IPR001240; STV_pkinase.
InterPro: IPR001245; TYr_pkinase.
Pfam: PF00069; pkinase; I.
SMART; SM00220; STRC; I.
SMART; SM00220; STRC; I.
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01-MAR-2001 (TrEMBLrel. 16, C:
01-MAR-2001 (TrEMBLrel. 19, Ls
01-DEC-2001 (TrEMBLrel. 19, Ls
PUTATIVE RECEPTOR KINASE:
P0698G03.26 OR P0494A10.4.
Oryza sativa (Rice).
                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-DEC-2001 (TrEMBLrel. 19,
                   :| :|: :|
609 EEVANRSQESKQESRSD 625
88 KEQRVYQEATKEVPTTD 104
                                                                                                                  PRELIMINARY;
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
A STRAIN-CV. NIPPONBARE;
A STRAIN-CV. NIPPONBARE;
A Corp. Sasaki T., Matsundto T., Yamamoto K.;
Corp. Sastiva nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0494A10.";
Clone:P0494A10.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP007247; BAB1742.1;
REMBL; AP007247; BAB1742.1;
REMBL; AP007247; BAB1742.1;
REMBL; AP007247; BAB1742.1;
REMBL; AP007241; BAB55464.1;
InterPro; IPR000719; Buk_pkinase.
InterPro; IPR0004040; STV_pkinase.
RICAPPO: IPR001245; TYT_pkinase.
RICAPPO: STRC; 1.
SMART; SM00219; TYTKC; 1.
                                                                                                   [1] SEQUENCE FROM N.A.
SETRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0698G03.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                            NCBI_TaxID-4530;
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	215 36.4 303 22 AA029304 Human 215 36.4 303 22 AAB87608 Human 215 36.4 714 21 AAY70209 Murino 185.5 31.4 1369 20 AAY24788 Human 185.5 31.4 1369 22 AA039009 Human	179.5 30.4 114 21 AAG03662 Human Secreted 179.5 30.4 192 22 AAU14154 Human novel pro 167 28.3 90 22 AAU14390 Human novel pro 157.5 26.7 98 21 AAX84900 A human prolife	100 16.9 21 22 AAB65128 Mouse 88.5 15.0 318 19 AAW69429 Human 86.5 14.7 287 20 AAY22236 Human	86.5 14.7 845 21 AAY49419	85.5 14.7 844 13 AAR25671 Mouse vay proto o	79.5 13.5 188 22 ABB10242 Human 79.5 13.3 1589 21 AAY66822 AMINO 78.5 12.3 46.9 17 AAMONGS95 Human 7.5 12.9 46.9 17 AAMONGS95 HUMAN	72 12.2 402 1/ ARY32158 72 12.2 1144 20 ARY32158 71 12.0 2091 21 AAB12000	70.5 11.9 663 19 AAW49872 Thermotoga 70.5 11.9 680 18 AAW44564 Thermotoga	70.5 11.9 680 70.5 11.9 680 70 11.9 280 70 11.9 1683	ALIGNMENTS	RESULT 1	ID AAB69126 standard; Protein; 110 AA.	AA AAB69126;	DT 23-APR-2001 (first entry)	Human MLP prote		cardiant; gene therapy; secretory cell inhibitor.	XX XX	PN WO200102564-A1. XX	PD 11-JAN-2001,	PA PA 29-JUN-2000; 2000WO-JP04278.	PR 30-JUN-1999; 99JP-0186718.	PA (TAKE) TAKEDA CHEM IND LTD.	PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K; PI Tanaka H;	XX XX	Safe,
4.5 Compugen Ltd.	: Search time 30.16 Seconds (without alignments) 405.110 Million cell updates/sec	RVYQEATKEVPTTDIDFFCE 110			5: 747574			!		genesegp-emb1/AA1984.DAT:* genesegp-emb1/AA1985.DAT:* genesegp-emb1/AA1985.DAT:*		/genesacyp cm2/cm1/cm1/cm1/cm1/cm1/cm2/cm2/cm2/cm2/cm2/cm2/cm2/cm2/cm2/cm2	નું €નું દ	<u> </u>	/geneseqp-emb1/AA1990.DA1:* /geneseqp-emb1/AA1997.DAT:*		/geneseqp-empi/AAZ001.DAT:*	ceed by chance to have a of the result being printed,			Description	Human MLP protein		se MLI	Rat MLP protein se Rat MLP protein se Rat MLP protein se	anoma inhibit an MIA protei
GenCore version pyright (c) 1993 - 2000	search, using sw model tember 23, 2002, 09:36:50	US-10-019-455A-24 590 1 HGIFMDRLASKKLCADDECV	BLOSUM62 Gapop 10.0 , Gapext 0.5	747574 segs, 111073796 residues	hits satisfying chosen parameters	length: 0 length: 200000000	Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Seneseq_032802:*	1: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AAL1980.DMT 2: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AAL981.DAT 3: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AAL982.DAT 4: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AAL983.DAT 4: /SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AAL983.DAT	: /SIDS1/gcgdata/hold-geneseq/c : /SIDS1/gcgdata/hold-geneseg/c : /SIDS1/gcgdata/hold-geneseg/c : /SIDS1/gcgdata/hold-geneseg/c	(SIDSI/gcgdata/hold-geneseq/collors) (SIDSI/gcgdata/hold-geneseq/collors)	7: /SIDSI/gogdata/hold-geneseq/	4: /SIDSI/gcgdata/notd-geneseq/ creft/fcgdata/hold-geneseq/	5: /SIDSI/gcgdata/mold-geneseq/	/: /SIDSI/gcgdata/noId-geneseg/ 8: /SIDSI/gcgdata/hold-geneseg/ 9: /SIDSI/gcgdata/hold-geneseg/	0: /SIDSI/gegdata/hold-geneseg/genesegp-embl/AA1999 1: /SIDSI/gegdata/hold-geneseg/genesegp-embl/AA2000	` }	s the number of results predict for than or equal to the score ved by analysis of the total	SUMMARIES		Match Length DB ID	00.0 110 22	00.0 128 22 00.1 108 22 95 1 105 22	7 110 22	91.7 110 22 AAB69131 91.7 128 22 AAB69130 70.7 87 22 AAB69129	.0 131 16 .0 131 22
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         \begin{array}{l} \texttt{A} \times \texttt{A} \times \texttt{C} \\ \texttt{
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                                                                                                                                                                                                                                                         The present invention describes novel MLP proteins and their encoding by MDAs. The MLP proteins and DNAs have antinflammatory and cardiant activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic angiogenesis. AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used in the exemplification of the present invention.
encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and joint
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24..128
/label- Mature_protein
/note- "separately claimed in Claim 10"
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100.0%; Score 590; DB 22;
Best Local Similarity 100.0%; Pred. No. 1.1e-68;
Matches 110; Conservative 0; Mismatches 0;
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                                                                                                                                                                            Claim 1; Page 97-98; 111pp; Japanese.
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02-MAY-2000; 2000US-0563786
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Peptide
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The present sequence is charton. The among a consideration of the present sequence is charton. The among a monoton sequence is predicted from a novel assembled cDNA (see AAH26343) based on Hyseq clone number 1637227. The protein has a mon. Wt. of 14 kba unglycosylated. GRLP belongs to the same protein family as growth regulatory proteins, growth factors, human melanoma derived growth regulatory proteins. Growth factors, human melanoma derived growth regulatory proteins. Growth factors inhibitory activity, cattle cartlinge-derived retinoic acid sensitive protein (CD-RAP, 44% identity and 64% inhibitory activity, cattle cartlinge derived similarity over 126 amino acids) and other retinoic acid sensitive proteins. GRLP polypeptides and polynucleotides of the invention can be used in the prophylaxis, treatment (including gene therapy) cartlinge development and maintenance, inhibition of melanoma cell growth and tumours, including neuroectodermal tumours such as and alfarentiation activity, stem cell growth factor activity, may also have nutritional uses, cytokine and cell proliferation or differentiation activity, stem cell growth factor activity, immunostimic activity, haemostatic and thrombolytic activity, use in cancer diagnosis and therapy, drug screening, receptor/ligand activity, antiinflammatory atthritis and inflammation.
                                                                           present sequence is that of a novel human growth regulatory-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 128;
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100.0%; Pred. No. 1.4e-68;
ive 0; Mismatches 0;
Claim 10; Page 116-117; 119pp; English.
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Best Local Similarity 100.
Matches 110; Conservative
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WO200102564-A1
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Màtches 105;
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                                                                                                                                        The present invention describes novel MLP proteins and their encoding by MLS. The MLP proteins and DNAs have antinflammatory and cardiant activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing to treating bone and joint diseases as well as pathologic angiogenesis. AAF$5003 to AAF$5099 and AAB$0122 to AAB$0122 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated human growth regulatory-like polypeptide useful for treating e.g. Alzheimer's disease, cancer, autoimmune disorders, hyperproliferative disorders, coagulation disorders, and nervous system
                                                              Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and joint
 Noguchi Y, Yoshimura K;
                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                         Human growth regulatory-like polypeptide (mature protein).
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                                                                                                                                                                                                                                                                       100.0%; Score 590; DB 22;
ilarity 100.0%; Pred. No. 1.4e-68;
Conservative 0; Mismatches 0;
 Mogi S,
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                                                                                                                   Claim 2; Page 91-92; 111pp; Japanese.
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Ohkubo
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02-MAY-2000; 2000US-0563786
 Ogi K,
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                              WPI; 2001-159271/16.
N-PSDB; AAF59065.
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Best Local Similarity
Matches 110; Conserv
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 Nishi K,
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           Tanaka H;
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polypeptide (GRLP) mature protein. The sequence is predicted from a novel assembled cDNA (see AAH26343) based on Hysaq clone number a novel assembled cDNA (see AAH26343) based on Hysaq clone number (16372272. The protein has a mol. Wt. of 14 kDa unglycosylated. GRLP belongs to the same protein family as growth regulatory proteins, growth factors, human melanoma derived growth regulatory proteins, or melanoma inhibitory activity, cattle cartilage derived retinoic acid sensitive protein (CD-RAP, 44% identity and 64% is amiliarity over 126 amino acids) and other retinoic acid sensitive protein (CD-RAP, 44% identity and 64% is similarity over 126 amino acids) and other retinoic acid sensitive protein (CD-RAP, 44% identity and 64% is amino acids) and oplynucleotides of the invention can be used in the prophylaxis, treatment (including gene therapy) and diagnosis of disorders and diseases caused by, or involving, cartilage development and maintenance, inhibition of melanoma cell growth and tumours, include the GRLP mature protein, cartilage development and maintenance inhibition of melanoma cell and contains. The polypeptides, which include the GRLP mature protein, cartilage development and maintenance inhibition of melanoma cell cartilage development and maintenance of the GRLP mature protein, cartilage development and maintenance of the GRLP mature protein, cartilage development and maintenance of the GRLP mature protein, cartilage development and maintenance of the contains and 
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                                                                                                             present sequence is that of a novel human growth regulatory-like
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100.0%; Pred. No. 6.2e-65;
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Claim 10; Page 117; 119pp; English.
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100.0%; Piv
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                                                                              Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and joint
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 Α.
 Yoshimura
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                                                                                                                                                                                                                                                                                                                                                                                                                     MLP; MIA; melanoma inhibitory activity; cancer; bone disease; joint disease; pathologic anglogenesis; diagnosis; antiinflammatory; cardiant; gene therapy; secretory cell function regulator; promoter;
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Pred. No. 4.4e-63;
7; Mismatches 4;
 Mogi S,
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Ohkubo S,
                                                                                                                                                  Claim 3; Page 98-99; 111pp; Japanese.
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ID AAB69125 standard; Protein; 128
                                                                                                                                                                                                                                                                                                                                               Match 92.7%;
Local Similarity 90.0%;
les 99; Conservative
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                                       WPI; 2001-159271/16
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N-PSDB; AAF59068.
Nishi K,
                                                                                                                                                                                                                                                                                                         110 AA;
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                                                       N-PSDB; AAF59080
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Tanaka H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nhibitor
              Tanaka H;
                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB69125;
                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                           diseases
Itoh Y,
                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                       The present invention describes novel MLP proteins and their encoding DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing to read and joint diseases as well as pathologic angiogenesis. AAF55063 to AAF55099 and AAB69122 to AAB69132 represent sequences used in the exemplification of the present invention.
   bone and joint
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Safe, low-toxicity secretory cell function-regulatory protein and encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and joint
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Noguchi Y, Yoshimura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes novel MLP proteins and their encoding DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant activities, and can be used in gene therapy and as secretory cell
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                 1 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MLP; MIA; melanoma inhibitory activity; cancer; bone disease; joint disease; pathologic angiogenesis; diagnosis; antiinflammatory; cardiant; gene therapy; secretory cell function regulator; promoter;
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                                                                                                                                                                                                                                                                                                                                                                        or treating e.g.
                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                     Score 547; DB 22;
Pred. No. 5.4e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mogi S,
                                                                                                                                                                                                                                                                                  7; Mismatches
and inhibitors for preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat MLP protein sequence SEQ ID NO:49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nishi K, Ogi K, Ohkubo S,
                                             Page 93-94; 111pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 5; Page 107; 111pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB69131 standard; Protein; 110
                                                                                                                                                                                                                                                      92.7%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99JP-0186718.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                      Query Match 92.7
Best Local Similarity 90.0
Matches 99; Conservative
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                                                                                                                                                                                                           128
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   promoters
diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inhibitor
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                                             Claim 4;
                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB69131;
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The present invention describes novel MLP proteins and their encoding MNAs. The MLP proteins and DNAs have antinflammatory and cardiant activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic angiogenesis. AAFS9063 to AAFS9099 and AAB69122 to AAB69132 represent sequences used in the exemplification of the present invention.
function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic angiogenesis.

AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MLP; MIA; melanoma inhibitory activity; cancer; bone disease; joint disease; pathologic anglogenesis; diagnosis; antiinflammatory; cardiant; gene therapy; secretory cell function regulator; promoter;
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                 1 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGA 60
                                                                                                                                                                                                                               ö
                                                                                                                                                  Length 110;
                                                                                                                                                                                                                                                                                                61 GEFWAGSVYGDGQDEMGVVGYFPRNLVKEQRVYQEATKEVPTTDIDFFCE 110
                                                                                                                                                                                  Indels
                                                                                                                                                                                 5;
                                                                 in the exemplification of the present invention.
                                                                                                                                                Score 541; DB 22;
Pred. No. 2.6e-62;
7; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat MLP protein sequence SEQ ID NO:47.
                                                                                                                                                                                                                                                                                                                                                                                                 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 106; 111pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                 standard; Protein; 128
                                                                                                                                                  91.7%;
89.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUN-2000; 2000WO-JP04278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                  Conservative
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                                                                                                                                                Query Match
Best Local Similarity
Matches 98; Conserv
                                                                                                   110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nishi K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inhibitor
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                                                                                                   Sequence
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Sequence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encoded DNA, applicable as drugs, in diagnosis and development of promoters and inhibitors for preventing or treating e.g. bone and joint diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yoshimura K;
                           Gaps
                                                                   MLP; MIA; melanoma inhibitory activity; cancer; bone disease; joint disease; pathologic angiogenesis; diagnosis; antiinflammatory; cardiant; gene therapy; secretory cell function regulator; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 DRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWA 65
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Length 128;
                                                                                                        61 GEFWAGSVYGDGQDEMGVVGYFPRNLVKEQRVYQEATKEVPTTDIDFFCE 110
                                                                                                                     Length 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Noguchi Y,
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                           Indels
Score 541; DB 22;
Pred. No. 3.3e-62;
7; Mismatches 5;
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Pred. No. 2.6e-46;
5; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s,
                         7; Mismatches
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                                                                                                                                                                                                                                                                                protein sequence SEQ ID NO:39.
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88.5%;
 91.7%;
89.1%;
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                                                                                                                                                                                                  AAB69129 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ogi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 88.5
les 77; Conservative
                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-159271/16.
             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JUN-2000;
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                                                                                                                                                                                                                                                     23-APR-2001
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                           98;
                                                                                                                                                                                                                                                                                                                                                   inhibitor
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 Query Match
Best Local 9
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Matches
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MIA; melanoma inhibiting activity protein; antiinflammatory; human; antiarthritic; antirheumatic; antithyroid; osteopathic; nephrotropic; immunosuppressive; ophthalmological; dermatological; antidiabetic; neuroprotective; immune tolarance; T-cell tolarance.
                                                                                                                                                                                                                                                                                                                                                                             Use of melanoma inhibiting activity protein or its derivatives as immune modulatory agents for the treatment of inflammatory diseases, specifically rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; Page 34; 41pp; English.
                                                                                                                                                                                                                                     15-MAR-2001; 2001WO-EP02991.
                                                                                                                                                                                                                                                             23-MAR-2000; 2000EP-0201063
                                                                  Human MIA protein sequence.
                                        07-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                       (ALKU ) AKZO NOBEL NV.
                                                                                                                                                                                                                                                                                                                                          2001-611446/70.
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N-PSDB; AAH47783.
                                                                                                                                                                                   WO200170253-A1.
                                                                                                                                                                                                                                                                                                                Nelissen RLH,
                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                           27-SEP-2001.
                AAG65614;
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m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This protein has melanoma-inhibiting activity and can be used to treat cancer (melanoma, glioblastoma, neuroblastoma, small cell lung aancer, neuroectodermal tumours) or as an immunosuppressant lung aancer, neuroectodermal tumours) or as an immunosuppressant peripheral blood lymphocytes). Antibodies raised against the protein can be used to detect cell producing the protein and also for protein purification. Probes derived from DNA encoding the protein (AAQ84050, AAQ84051) can be used to detect sequences encoding the protein (AAQ84050, AAQ84051) can be used to detect sequences encoding the protein (AAQ84050, CAAQ84050).
                                                                                                                                                                                           Melanoma; inhibition; cancer; melanoma; glioblastoma; neuroblastoma; small cell lung cancer; neuroectodermal tumours; immunosuppressant; phytohaemagglutinin; lymphocyte; interleukin 2; IL-2; detection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New melanoma inhibiting protein and related nucleic acid -
vectors, transformed cells, antibodies etc., useful for treating
tumours and as immunosuppressant e.g. by gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33; Indels
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Pred. No. 8.7e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21; Mismatches
                                                                                                                                                                   Melanoma inhibiting protein (human).
 92
                     87
                                                                                       AAR69811 standard; Protein; 131 AA.
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             61 gsvygdhqdemgivgyfpsnlvreqrv
                                                                                                                                                                                                                                                                                                                                                                                         (BOEF ) BOEHRINGER MANNHEIM GMBH.
66 GSVYGDGQDEMGVVGYFPRNLVKEQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 54; 85pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43.0%;
45.4%;
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                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                   probe; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-075191/10
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Best Local Similarity
Matches 49; Conserv
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                                                                                                                                          26-0CT-1995
                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                      19-JUL-1994;
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                                                               RESULT 10
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Verheilden GFM;

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protein and/or its fragments that have anti-inflammatory effects and induce systemic immune tolerance or specific T-cell tolerance to MIA antigen. for manufacturing a preparation is inflammatory diseases and for induction of systemic immune tolerance or specific T-cell tolerance in patients suffering from or susceptible to inflammatory diseases. A fragment of MIA is useful as a therapeutic substance and is useful for manufacture of pharmaceutical preparations against inflammatory diseases such as an immune-cell mediated cartilage of destruction disease, specifically rheumatorid arthritis, autoimmune diseases like Graves disease, juvenile arthritis, primary glacuses, systemic lupus erythematosis, inflammatory bowel disease, mustiple sclerosis or diabetes. The MIA polypeptides have specific effect on the autoreactive T-cells thus leaving the other components of the immune system intact as compared to the non-specific suppressive effect of immunosuppressive drugs. The present sequence represents a
The invention relates to the use of melanoma inhibiting activity (MIA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 WAGSVYGDGQDEMGV-VGYFPRNLVKEQRVYQEATKEVPTTDIDFFCE 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43.0%; Score 253.5; DB 22;
45.4%; Pred. No. 8.7e-25;
tive 21; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 AA;
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Melanoma; inhibition; cancer; melanoma; glioblastoma; neuroblastoma; small cell lung cancer; neuroectodermal tumours; immunosuppressant; phytohaemagglutinin; lymphocyte; interleukin 2; IL-2; detection; probe; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treat cancer (melanoma, glioblastoma, neuroblastoma, small cell lung cancer, neuroectodermal tumours) or as an immunosuppressant (it inhibits IL-2 or phytoheamagglutinin induced proliferation of peripheral blood lymphocytes). Antibodies raised against the protein can be used to detect cell producing the protein and also for protein (AAQ84052) can be used to detect sequences encoding the protein (AAQ84052) can be used to detect sequences encoding the protein or related proteins. The protein may be expressed as a fusion protein (conjugated with dihydrofolate reductase (DHFR)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New melanoma inhibiting protein and related nucleic acid -vectors, transformed cells, antibodies etc., useful for treating tumours and as immunosuppressant e.g. by gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This protein has melanoma-inhibiting activity and can be used to
                                                                                                                                                                    Melanoma inhibiting protein (murine).
                           AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kaluza B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BOEF ) BOEHRINGER MANNHEIM GMBH.
AAR69812
ID AAR69812 standard; Protein; 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; Page 60; 85pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93DE-4324247.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94WO-EP02369.
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                                                                                                                       (first entry)
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Best Local Similarity 43.58
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bogdahn U, Buettner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1995-075191/10.
N-PSDB; AAQ45052.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 AA;
                                                                                                                       26-OCT-1995
                                                                                                                                                                                                                                                                                                                                        Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                  WO9503328-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  02-FEB-1995.
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                                                                          AAR69812;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to the use of melanoma inhibiting activity (MIA) protein and/or its fragments that have anti-inflammatory effects and induces systemic immune tolerance or specific T-cell tolerance to MIA antigen, for manufacturing a preparation against inflammatory diseases and for induction of systemic immune tolerance or specific T-cell tolerance in patients suffering from or susceptible to inflammatory diseases. A fragment of MIA is useful as a therapeutic substance and is useful for manufacture of pharmaceutical preparations against inflammatory diseases such as an immune-cell mediated cartilage destruction disease, specifically rheumatoid arthritis, autoimmune diseases like Graves' disease, juvenile arthritis, primary glomerulonephritis, polyarthritis, osteoarthritis, Sjogren's syndrome, myasthenia graveis, addison's disease, primary bilary sclerosis, uveitis, systemic lupus erythematosis, inflammatory bowel disease, multiple sclerosis or diabetes. The MIA polypeptides have specific effect on the autoreactive T-cells thus leaving the other components of the immune system intact as compared to the non-specific suppressive effect of immunosuppressive drugs. The present sequence represents a compared to the non-specific suppressive converted and a human recombinant MIA(his7) protein.
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                                                                                                                                                                                        MIA; melanoma inhibiting activity protein; antiinflammatory; human; antiarthitic; antirheumatic; antithyroid; osteopathic; nephrotropic; immunosuppressive; ophthalmological; dermatological; antidiabetic; neuroprotective; immune tolerance; T-cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of melanoma inhibiting activity protein or its derivatives as immune modulatory agents for the treatment of inflammatory diseases, specifically rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.6%; Score 251.5; DB 22;
45.8%; Pred. No. 1.7e-24;
live 20; Mismatches 33;
                                                                                                                                           human MIA(his7) protein.
  AAG65615 standard; Protein; 137 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 35; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Verheijden GFM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000EP-0201063.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-MAR-2001; 2001WO-EP02991.
                                                                                              (first entry)
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Best Local Similarity 45.8
Matches 49 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ALKU ) AKZO NOBEL NV
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                                                                                                                                                                                                                                                                                                                                                          WO200170253-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nelissen RLH,
                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                              07-JAN-2002
                                                                                                                                             Recombinant
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                                                 AAG65615;
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3,
                                      Gaps
                                                                           5 MDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGE-F 63
                                                                                            5,
   Length 130;
                                                                                                                                                                       39.2%; Score 231.5; DB 16; Length 43.5%; Pred. No. 6.3e-22; Live 21; Mismatches 35; Indels
                                                                                                                                                    64 WAGSVYGDGQDEMGV-VGYFPRNLVKEQRVYQEATKEVPTTDIDFFCE 110
                                                                                                                                                                                                                                                                                                                                                                                                Human protein sequence SEQ ID NO:1349.
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immunodeficiency virus;

AAM25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antinifammatory; antirheumatic; cells they are expressed in, such as: antinifammatory; antirheumatic; antiatrhritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; antiadicade; antimutagen; cardiavascular; antianaemic; antiaggregant; heemostatic; vulnerary; antitiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; and immunostimulant. The proteins and polynucleotides are useful for screening for sproduction, The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, heematopoietic disorders, osteoporosis, severe combined immunodeficiency, eczema, allergic channel, ad disease, Parkinson's disease, neurodegenerative and parchare. Humani cancer; uter; nay intercruti, numen inmicoretateury virus; antibacterial; endocrine; cardiant; central nervous system; virucide; antibacterial; endocrine; cardiant; central nervous system; virucide; antibacterial; endocrine; cardiavascular; antianaemic; anaemia; antiangular; haemostatic; vulnerary; antiulcer; osteopathic; eczema; dermatological; antialerary; antiulcer; osteopathic; cezema; dermatological; antidalerary; antiulcer; antidabetic; cytostatic; neuroprotective; antidaperssant; nootropic; antidarkinsonian; infection; immunostimulant; gene therapy; antisense therap; vaccine; inflammation; antidapphiactic; rheumatolog arthritis; septic shock; pancreatitis; cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; enhombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression; allergic rhinitis; diabetes; neurodegenerative disorder; Isolated human polynucleotides encoding polypeptides, useful for treatment and diagnosis of e.g. cancer, ulcers and HIV infection infection; Claim 20; Page 279; 1217pp; English. Tang YT, Liu C, Drmanac RT; 23-DEC-1999; 99US-0471275. 21-JAN-2000; 2000US-0488725. 25-APR-2000; 2000US-0552317. 22-DEC-2000; 2000WO-US35017 neurological disorder. WPI; 2001-457603/49. (HYSE-) HYSEQ INC. N-PSDB; AAH99775 WO200153455-A2 Homo sapiens. 26-JUL-2001

138 AA; Sequence

neurological disorders

э; Э Gaps . 6 DB 22; Length 138; 34; Indels Query Match 38.4%; Score 226.5; DB 2 Best Local Similarity 44.7%; Pred. No. 3.1e-21; Matches 46; Conservative 14; Mismatches 34

7 RLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAG 66

ò Db

TANGO 130; human; hTANGO130; Melanoma-inhibiting protein; MIA; marker; chromosome 4p1; chromosome 7; chromosome 14p1; tumour; cytostatic; immunomodulatory; cell proliferation/differentiation; chondrosarcoma; malanoma; diagnosis; epithelium; mesenchyma; carcinoma; glioblastoma; midolator; cell.cell interaction; metastasis; cell migration; retinoic acid; AP2 transcription factor; morphogenesis; embryonic cell growth. 74..410 /label= Mature_human_TANGO_130_protein /note= "This region is specifically claimed" 1..125 /label- MIA_homology_domain /note- "Homologous by 38% to human MIA" 67 SVYGDGQDEMGVVGYFPRNLVKEQRVYQEATKEVPTTDIDFFC 109 1..23 /label- Signal_peptide Location/Qualifiers AAY70210 standard; Protein; 410 AA. 06-JUN-2000 (first entry) Human TANGO 130 protein. WO200012762-A1. Homo sapiens. AAY70210; Key Peptide Protein Domain 15 ŏ 염

99WO-US20032 01-SEP-1999; 09-MAR-2000.

(MILL-) MILLENNIUM BIOTHERAPEUTICS INC. 98US-0145056. 01-SEP-1998;

Pan Y;

WPI; 2000-237889/20. N-PSDB; AAZ51245 Nucleic acids encoding human and murine TANGO 130, a melanoma-inhibiting protein homolog, useful for modulating cell proliferation and differentiation -

Claim 9; Fig 3; 128pp; English.

The present amino acid sequence is the human TANGO 130 protein

(hTANGO130). The gene is mapped to chromosomes 4pl, 7, 14q and 18pl.

(human TANGO 130) has highest expression in testis and also in heart, brain, placenta, liver, lung, skeletal muscle, pancreas, kidney, spleen, thymus, prostate and uterus. It has cytostatic and immunomodulatory activity. TANGO 130, a homologue of melanoma-inhibiting protein (MIA), inhibits growth of melanocytes and may be used to treat malignant melanomas, chondrosarcomas and metastatic tumours. They serve as serum markers for diagnosis and mentastatic tumours. They serve as serum markers for diagnosis and mentastatic tumours. They serve as serum markers for diagnosis and monitoring disease states. TANGO 130 inhibits abnormal or malignant proliferation of cells of the heart, liver, testis, kidney, immune system, CNS, skeleton, epithelial cells (e.g. carcinomas and melanomas). It modulates cell-cell interactions (e.g. call adhesion or cell-substrate interactions), cell migration (e.g. abnormal migration and metastasis of tumour cells), cell differentiation, rethiod acidemediated functions/activities, like modulation of AP2 transcription

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factor function and embryonic cell growth/morphogenesis.
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410	
Sequence	
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9; Gaps
 Query Match
 38.2%;
 Score 225.5;
 DB 21;
 Length 410;

 Best Local Similarity 44.7%;
 Pred. No. 1.9e-20;
 Matches 46;
 Conservative 14;
 Mismatches 34;
 Indels 9;

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rch completed: September 23, 2002, 09:37:53 time: 63 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compu	OM protein - protein search, using sw model	23, 2002, 09:36:50	Title: US-10-019-455A-24 Perfect score: 590 Sequence: 1 HGIPMDRLASKKICADDECV	table: BLOSUM62 Gapext 0.5	Sarched: 231628 seqs, 24425594 residues	cal number of hits satisfying chosen parameters	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 08 Maximum Match 1008 Listing first 45 summaries	Database: Issued_Patents_AA:* 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:* 2: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:* 3: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:* 4: /cgn2_6/ptodata/2/iaa/BCOMB.pep:* 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:% 6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:	Pred. No. is the number of results predicted by score greater than or equal to the score of the and is derived by analysis of the total score d	SUMMARIES	Result Ouery No. Score Match Length DB ID	253.5 43.0 131 1 US-0	81.5 13.8 54 4 US-0 78.5 13.3 1589 3 US-0	72.5 12.3 48 4 US-0 72 12.2 462 4 US-0	66.5 11.3 642 2 US-01 66.5 11.3	66 11.2 248 4 US-0 66 11.2 280 1 US-0 66 11.2 280 1 US-0	66 11.2 280 1 US-0 66 11.2 280 1 US-0	66 11.2 280 4 US-0 66 11.2 280 4 US-0 66 11 2 370 1 US-0	66 11.2 370 1 0S-0 66 11.2 370 1 0S-0 66 11.2 370 1 0S-0 66 11.2 370 1 0S-0	22 66 11.2 397 1 0S-08-434-255-2 23 66 11.2 397 1 0S-08-434-255-4 24 66 11.2 397 1 0S-08-434-255-4 25 66 11.3 397 1 0S-08-439-967-2	66 11.2 397 1 US-00 66 11.2 397 1 US-00
4.5 Compugen Ltd.		; Search time 12.89 Seconds (without alignments) 208.442 Million cell updates/sec	RVVOEATKEVPTTDIDEFCE 110	ļ.		s: 231628	E 2 :		B.pep:* B.pep:* B.pep:* Combine pep:* Combine pep:*	cted by chance to have a ; of the result being printed, ; score distribution.		Description	Sequence	eodnebes eodnebes eodnebes	Sequence	Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence	Sequence	Sequence	Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli	Sequence 4, Appli Sequence 4, Appli
28 66 11.2 30 66 11.2 30 66 11.2 31 65 11.0	6 6 4	0000	64 44 44 44	63.5 63 63	63		RESULT 1	-08-5/8-649-2 Sequence 2, Appropriate No. 577 GENERAL INFOI	APPLICANT: Ulrich Bogdan APPLICANT: Reinhard Buttner APPLICANT: Brigitte Kaluza TITLE OF INVENTION: MELANOM NUMBER OF SEQUENCES: 24 CORRESPONDENCE ADDRESS: ADDRESSEE: Relfe & Lynch STREET: 805 Third Avenue	CITY: New York STATE: New York COUNTRY: USA ZIP: 10022	ADABL PE:	COMPUTER: IBM PS/Z OPERATING SYSTEM: PC- SOFTWARE: Wordperfect	APPLICATION NUMBER: US FILING DATE: 29-July-	CLASSIFICATION: 433 PRIOR APPLICATION DATA: APPLICATION NUMBER: DE P 43	FILING DATE: 20-3 ATTORNEY/AGENT INFOR	NAME: ANGIEW L. TIAJOLO REGISTRATION NUMBER: 31, REFERENCE/DOCKET NUMBER:	TELECOMMUNICATION INFORMATION TELEPHONE: (212) 688-9200 TELEFAX: (212) 838-3884	INFORMATION FOR SEQ ID NO SEQUENCE CHARACTERISTIC	LENGTH: 131 amino acid TYPE: amino acid	OS-578-649-2	Query Match Best Local Similarity 45.	5 MDRLASKKLCADDEC
397 1 US-08-459-871-2 397 1 US-08-459-871-4 509 4 US-08-630-915A-194 57 4 US-08-630-915A-136	. ⊢ .		4 W 4 R	444	Ŋ	ALIGNMENTS		US/08578649	rich Bogdan zinhard Buttner iigitte Kaluza TION: MELANOMA-INHIBITING PROTEIN FENCES: 24 ? ADDRESS: Felfe & Lynch	į	JE FORM: 3.5 inch 1.44 Mb storage diskette	PC-DOS fect	NUMBER: US/08/578,649 29-July-1994	33 TA: :: DE P 43 24 247.2	uly-1993 MATION:	TIAJOIOII 3ER: 31,575 NUMBER: BOER 1035-PFF/ALT	IFORMATION: 688-9200 8-3884	NO: 2:	acids	ein	0%; Score 253.5; DB 1; 4%; Pred. No. 1.9e-25; 21. Mismatches 33.	SLASAQEDYNAPDCRFINVKKGQQIY
Sequence 2, Appli Sequence 4, Appli Sequence 194, Appli Sequence 136, App	Sequence 219, Appl Sequence 20, Appl	Sequence 11, Appl Sequence 10, Appl Sequence 10, Appl Sequence 12, Appl Sequence 12, Appl		210, 125, 14,	14,																Length 131;	63 8

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CORRESPONDENCE ADDRESS:
    NUMBER OF SEQUENCES:
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LENGTH: 54
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5 MDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQOIYVYSKLVKENGAGE-F 63 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 
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                                                                                                                  64 WAGSVYGDGQDEMGV-VGYFPRNLVKEQRVYQEATKEVPTTDIDFFCE 110
                                                                                                                                                                 64 WAGSVYGDGQDEMGV-VGYFPRNLVKEQRVYQEATKEVPTTDIDFFCE 110
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COMPUTER: 1BM PS/2
COMPUTER: 1BM PS/2
COMPUTER: 1BM PS/2
COPERATIOS SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 24 247.2
FILING DATE: 20-July-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/08578649
Patent No. 5770366
GENERAL INFORMATION:
APPLICANT: Ulrich Bogdan
APPLICANT: Brighte Kaluza
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
NUMBER OF SEQUENCES: 24
CORRESSONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/07646537B
Patent No. 5348864
GENERAL INFORMATION:
APPLICANT: Barbacid, Mariano
TITLE OF INVENTION: Vav Proto-Oncogene Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Andrew L. Tiajoloff
REGISTRATION NUMBER: 31,575
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 688-3884
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Felfe & Lynch
805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein 3-08-578-649-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 805 Third
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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ZIP: 10022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-07-646-537B-2
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US-08-578-649-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-346-510B-21
Sequence 21, Application US/09346510B
Sequence 21, Application US/09346510B
Sequence 21, Application US/09346510B
Sequence 21, Application:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Wang, Yinxiang
TITLE OF INVENTION: SH3-Containing Protein, DNA and Uses Thereof
FILE REFERENCE: D6221CIP
CURRENT APPLICATION NUMBER: US/09/346,510B
CURRENT APPLICATION NUMBER: 08/871,732
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 3999-07-03
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 14.5%; Score 85.5; DB 1; Length 844; Best Local Similarity 31.4%; Pred. No. 0.021; Matches 22; Conservative 14; Mismatches 21; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.8%; Score 81.5; DB 4; Length 54; 32.3%; Pred. No. 0.0015; tive 13; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Domain
CTHER INFORMATION: amino acid sequence of Vav SH3 domain
US-09-346-510B-21
                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/646,537B
FILING DATE:
CLASSIFICATION: 435
ADDRESSEE: Bristol-Myers Squibb Company STREET: P.O. Box 4000 CITY: Princeton
                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Gaul, Timothy J.
REGISTRATION UNDBER: 33.111
REFERENCE/DOCKET NUMBER: DC10
TELECOMMUNICATION INFORMATION:
TELEFONE: (609) 921-5901
TELEFAX: (609) 921-5901
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 844 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 32.3%
                                                  CITY: Princeton
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 08543-4000
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-07-646-5378-2
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STREET:
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                                                                                                                                                                                                                                 Sequence 4, Application US/09356952

Patent No. 611763

GENERAL INFORMATION:
APPLICANT: Borlack-Sjodin, Ann
APPLICANT: Borlack-Sjodin, Ann
APPLICANT: Borlack-Sjodin, Ann
APPLICANT: Cule, Philip
APPLICANT: Soft Engles (00-1-228)
CURRENT APPLICATION NUMBER: Col/093,631
EARLIER FILING DATE: 1998-07-21

NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 4

LENGTH: 1589
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OTHER INFORMATION: amino acid sequence of Vav SH3 domain at position 2
OTHER INFORMATION: through position 49 of SEQ ID No. 6281014 21
                       11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 LASKKLCADDECVYTISLASAQEDYNAP----DCRFINVKKGQQIYVYSKLVKENGAGE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 LSSSPSTSELTSIRPIGIVVAAYDFNYPIKKDSSSQLLSVQQGETIYILNK----NSGG- 99
28 AQEDYNAPDCRFINVKKGOQIYVYSKLVKENGAGEFWAGSVYGDGODEMGVVGYFPRNLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: O'Brien, Timothy J.
APPLICANT: O'Brien, Timothy J.
APPLICANT: Wang, Yinxiang
TITLE OF INVENTION: SH3-Containing Protein, DNA and Uses Thereof
FILE REFERENCE: D622ICIP
CURRENT APPLICATION NUMBER: US/09/346,510B
CURRENT FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: 08/871,732
PRIOR FILING DATE: 1997-06-09
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 24
LENGTH: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1589;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.3%; Score 78.5; DB 3; ilarity 25.8%; Pred. No. 0.42; Conservative 21; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 WWDGLVIDDSNGKVN-RGWFPQNFGRPLR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 FWAGSVYGDGQDEMGVVGYFPRNLVKEQR 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 24, Application US/09346510B
Patent No. 6281014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Saccharomyces cerevisiae US-09-356-952-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Domain
LOCATION: 2...49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-346-510B-24
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                                                                                                                                                                                                RESULT 5
US-09-356-952-4
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Patent No. 6309820
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: KAY, Brian K.
APPLICANT: FORWIRES, Dana M.
APPLICANT: FORWIRES, Dana M.
APPLICANT: FORWIRES, Dana M.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND TITLE OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 AAKPVVSGEEIAQVIA----SYTATGPEQLTLAPGQLI-----LIRKKNPGGWWEGEL 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16; Gaps
                                                 Gaps
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                                                                                                                  11;
                                                                                           31 DYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYFPRNLV
    Length 48;
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;; Pred. No. 0.53;
19; Mismatches 39; Indels
  12.3%; Score 72.5; DB 4; Length 4(
31.6%; Pred. No. 0.019;
tive 11; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/630,915A FILING DATE: 03-APR-1996 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 YGDGQDEMGVVGYFPRNLVKEQRVYQEATKEVPTTD 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          359 QARGKKRQ--IGWFPANYVK---LLSPGTSKITPTE 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSEE: Pennie & Edmonds LLP
F: 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1101-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 38:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 11 TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.2%;
22.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 462 amino acids TYPE: amino acid
Ouery Match
Best Local Similarity 31.69
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 12.2%
Best Local Similarity 22.9%
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-630-915A-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New York
COUNTRY: USA
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                     RESULT 7
US-08-630-915A-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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OTHER INFORMATION: NOTE: the reference contains a OTHER INFORMATION: sequence error; the correct sequence shown below is obtain OTHER INFORMATION: from GENBANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :::|:|| :: :: :: |:: |: | : || | | : | : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : || : 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         365 TFGDLVAAQLPAYGDEWKGVNLADGQD-----GLF--NADKAKAEFRKAKKALEADGVQF 417
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US-08-600-993A-48
; Sequence 48, Application US/08600993A
; Patent No. 5981229
; GENERAL INFORMATION:
    APPLICANT: Masure, H Robert
    APPLICANT: Pearce, Barbara J
    APPLICANT: Pearce, Elaine
    TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND
    TITLE OF INVENTION: ACELLULAR VACCINES BASED THEREON
                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/245,511
FILING DATE: 18-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
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ER: 600-1-069 CIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 18-MAY-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/116,541
FILING DATE: 01-SEP-1994
ATTONEY/AGENT INFORMATION:
ATTONEY AFFORMATION A
       411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 201 343-1684
TELEX: 1332321
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 642 amino acids
TYPE: amino acids
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PUBLICATION INFORMATION:
AUTHORS: Alloing, et al.
JOURNAL: Mol. Microbiol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                 New Jersey
: USA
                                            Hackensack
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DATE: 1990
US-08-245-511-48
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VOLUME:
                                                                             STATE: N
COUNTRY:
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;
                                                                                                                                     APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFFWAN, No. 6309820h
APPLICANT: HOFFWAN, No. 6309820h
APPLICANT: KAY, Brian K.
APPLICANT: KAY, Bana M.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
TITLE OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Sequence 48, Application US/08245511

GENERAL INFORMATION:

APPLICANT: Masure, H Robert

APPLICANT: Pearce, Barbara J

APPLICANT: Tuomanen, Blaine

TITLE OF INVENTION: ACELLULAR VACCINES BASED THEREON

TITLE OF SEQUENCES: 58

CORRESPONDENCES: ADDRESS:

ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1101-174
                                 Sequence 135, Application US/08630915A Patent No. 6309820 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 1101-1
REFERENCE/DOCKET NUMBER: 1101-1
TELECOMMUNICATION INFORMATION:
TELEPAX: (212) 790-9090
TELEPAX: (212) 869-8864/9741
TELEX: 6641 PENNIE
INFORMATION FOR SEQ ID NO: 135:
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LENGTH: 62 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 26.6
Matches 17; Conservative
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MOLECULE TYPE: peptide
US-08-630-915A-135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
US-08-630-915A-135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
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ADDRESSEE: No. 56210890 No. 5621089disk of No. 5621089th America, Inc. STREET: 405 Lexington Avenue, 64th Floor CITY: New York STATE: New York
                 APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFPAN, No. 6309820h
APPLICANT: HOFPAN, No. 6309820h
APPLICANT: HOFPAN, No. 6309820h
APPLICANT: MCCONNELL, Stephen J.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND TITLE OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 AQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGYFPRNLV 87
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                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 10036-2711
COMPUTER READBLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03.3-APR-1996
CLASSIFICATION: 536
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Patent No. 5621089;
GENERAL INFORMATION:
APPLICANT: Sloma, Alan P.
APPLICANT: Outtrup, Helle
APPLICANT: Dambmann, Claus
APPLICANT: Asslyng, Dorrit
TITLE OF INVENTION: ALKALINE PROTEASE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                         E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (212) 790-9090
TELERAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Miscrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/POCKET NUMBER: 11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88 KEQRVYQEATKEVPTTDID 106
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                                                                                                                                                                                                                                                                                                        CITY: New York
STATE: New York
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US-08-434-255-8
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AUTHORS: Alloing, et al.
JOURNAL: Mol. Microbiol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             309 EKVATKKALLNKDFRQALNFALDRSAYSAQ----INGKDGAALAVRNLFVKPDFVSAGEK 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 DRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKEN----- 58
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                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600,993A
FILING DATE: 1-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26,742
ER: 600-1-069 US
                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1-MAR-1996
CLASSIPECATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/245,511
FILING DATE: 18-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNDERR: US 08/116,541
FILING DATE: 01-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
ORGANISM: Streptococcus pneumoniae
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-630-915A-40; Sequence 40, Application US/08630915A; Patent No. 6309820
       STREET: Klauber & Jackson STREET: 411 Hackensack Avenue CITY: Hackensack STATE: New Jean Comment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELERAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 642 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Jackson Esg., David A. REGISTRATION NUMBER: 26,742 REPERENCE/DOCKET NUMBER: 600 TELECOMMUNICATION INFORMATION: 201487-5801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown
MOLECULE TYPE: peptide
AVPOTHETICAL: NO
                                                                                                                                    COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                      CORRESPONDENCE ADDRESS:
SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 27: Conserval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; PAGES: |633-644
; DATE: 1990
US-08-600-993A-48
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E: No. 5622850o No. 5622850d1sk of No. 5622850th America, Inc. 405 Lexington Avenue, 64th Floor
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                                                                                                                                                                                                                                                                                                    Query Match 11.2%; Score 66; DB 1; Length 280; Best Local Similarity 29.6%; Pred. No. 1.6; Matches 21; Conservative 11; Mismatches 39; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New JOINTRY: USA

COUNTRY: USA

ZIP: 10174-6401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION UNDBER: US/08/460,327
FILING DATE: 02-UNN-1995

*** ASSTPTCATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Sloma, Alan P.
APPLICANT: Outtrup, Helle
APPLICANT: Dambmann, Claus
APPLICANT: Dambmann, Claus
APPLICANT: Asslyng, Dorrit
ITILE OF INVENTION: ALKALINE PROTEASE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION UNBER: US 08/434,255

FILING DATE: 03-MAY-1995

ATTORNEY/AGENT INFORMATION:

NAME: AGISTRATION NUMBER: 34,086

REFERENCE/DOCKET NUMBER: 3764,400-US

RELEPHONE: 212-867-0123

TELEPHONE: 212-867-0123

TELEPHONE: 212-867-0123

TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 280 amino acids

TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.2%; Score 66;
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US-08-460-327-8
; Sequence 8, Application US/08460327
; Patent No. 5622850
  TELECOMMUNICATION INFORMATION
TELEPHONE: 212-867-0123
TELEPAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                  LENGTH: 280 amino acids TYPE: amino acid
                                                                                                                                                                    ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-459-967-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-460-327-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 TISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGY 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 11.2%; Score 66; DB 1; Length 280; Best Local Similarity 29.6%; Pred. No. 1.6; Matches 21; Conservative 11; Mismatches 39; Indels
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APPLICATION NUMBER: US/08/459,967
FILING DATE: 02-JUN-1995
CLASSIFICATION 435
PROOR APPLICATION NUMBER: US 08/434,255
FILING DATE: 03-MAY-1995
ATTON NUMBER: US 08/434,255
ATTON NUMBER: US 08/434,255
ATTON NUMBER: 33-MAY-1995
ATTON NUMBER: 33-MAY-1995
ATTON NUMBER: 33-MAY-1995
NAME: AGIST NUMBER: 34,086
ZIP: 10174-6401

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,255
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/08459967; Sequence 8, Application US/08459967; Patent No. 5622841
GENERAL INFORMATION:
APPLICANT: Sloma, Alan P.
APPLICANT: Duttrup, Helle
APPLICANT: Dambmann, Claus
APPLICANT: Asslyng, Dorrit
TITLE OF INVENTION: ALKALINE PROTEASE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 56228410 NO efficiency
                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: AGIS Dr., Cheryl H.
RECISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3764.400-US
TELECOMUNICATION INFORMATION:
TELEPAX: 212-867-0123
TELEPAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 280 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) MOLECULE TYPE: protein US-08-434-255-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA ZIP: 10174-6401 COMPUTER READABLE FORM:
                                                                                                                                                                                                                            CLASSIFICATION: 435
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GENERAL INFORMATION:
APPLICANT: Sloma, Alan P.
APPLICANT: Outtrup, Helle
APPLICANT: Dambmann, Claus
APPLICANT: Dambmann, Claus
APPLICANT: Dambmann, Claus
APPLICANT: Asalyng, Dorrit
TITLE OF INFORTION: ALKALINE PROTEASE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSE: No. 56503260 No. 5650326disk of No. 5650326th America, Inc.
CITY: New York
STREE: New York
COUNTRY: New York
COUNTRY: USA
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                        0; Gaps
                                                                                        22 TISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGY 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

11.2%; Score 66; DB 1; Length 280;
Best Local Similarity 29.6%; Pred. No. 1.6;
Matches 21; Conservative 11; Mismatches 39; Indels
1 Similarity 29.6%; Pred. No. 1.6;
21; Conservative 11; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:

ADDIUM TYPE: Floppy disk
COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OFFRATIG SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,871
FLING DATE: 02-JUN 1995
CLASSIFICATION NUMBER: US/08/459,871
FLING DATE: 03-MAY-1995
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3764.400-US
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-0123
INFORMATION POR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                         RESULT 15
US-08-459-871-8
Sequence 8, Application US/08459871
Patent No. 5650326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 280 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-459-871-8
                                                                                                                                                                                      94 APDTKILAVRV 104
Best Local Similarity
Matches 21; | Conserve
                                                                                                                                                  82 FPRNLVKEORV 92
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94 APDTKILAVRV 104

82 FPRNLVKEORV 92

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Search completed: September 23, 2002, 09:38:12

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22 TISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKENGAGEFWAGSVYGDGQDEMGVVGY 81 |::: : || || : : || || 34 TVAVLDSGVDYNHPDLARKVIKGYDFIDRDNNPMDLNGHGTHVAGTVAADTNNGIGVAGM 93

Job time: 82 sec